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Result
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   389.5
377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-938-901A-2
1701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MEAWRKALLAWYRENARPLP......VLRKALPLLAHAGVVPLPDA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

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5: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/pubpaa/US09A PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10A PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10 NEW PUB.pep:*
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                                                                   482
474
188
313
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1719
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_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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US-10-289-762-421

2 US-10-425-114-68280

6 US-10-437-963-138271

US-10-629-951-36

4 US-10-156-761-12241

US-09-738-626-6433
                                                                                                   US-10-437-963-103808
US-10-424-599-248081
US-10-629-951-34
US-10-335-977-7283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1351062
                                                                                                                                                            Sequence 2, Appli
Sequence 1326, App
Sequence 421, App
Sequence 68280, A
Sequence 138271,
Sequence 136, Appl
Sequence 12241, A
Sequence 12241, A
Sequence 6433, Ap
Sequence 6433, Ap
Sequence 248081,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
Sequence 34, Appl
Sequence 7283, Ap
Sequence 7282, Ap
Sequence 7279, Ap
Sequence 7280, Ap
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45	44	43	42	41	40	39	38	37	36						30	29	28										18	17	16
110.5	111	•	112.5		118.5	119		125.5	•	126	128	128	129.5	129.5	130	137.5	145	147.5	150	155	155	158.5	163.5	176	176.5	184.5	191	199	200.5
6.5	6.5	6.6	6.6	6.9	7.0	7.0	7.1	7.4	7.4	7.4	7.5	7.5	7.6	7.6	7.6	8.1	8 . 5	8.7	8.8	9.1	9.1		9.6	10.3	10.4	10.8	11.2	11.7	11.8
457	1729	1332	440	1072	416	187	776	6238	148	272	461	281	5245	170	158	184	211	260	373	393	172	355	304	259	90	310	185	268	214
12	10	10	12	16	12	12	12	16	16	15	14	14	14	16	12	15	9		12	16	12	15	12	15	11	14	5		12
US-10-282-122A-44928	4	US-09-840-743-11		US-10-437-963-114893	US-10-425-114-43512	US-10-425-114-68053	US-10-425-114-70995	US-10-343-710-71	7-701-	-493-1329	US-10-128-714-8128	-10-128-714-		US-10-767-701-39640	-10-424-599-		US-09-912-020-296	US-09-738-626-3828	_	\mathbf{r}	US-10-424-599-150617	Ļ	US-10-424-599-280749	US-10-369-493-5691	US-09-864-408A-9042	US-10-156-761-12127	US-10-629-951-35	US-09-864-866-43	US-10-335-977-7461
Sequence 44928, A	N		71	114893,	43512		Sequence 70995, A		Sequence 61161, A	Sequence 13299, A	e 8128,	312	11, Ar	396		Sequence 33, Appl		3828,	65596	113667,		æ	280749	O	9042,	Sequence 12127, A	L	3	Sequence 7461, Ap

ALIGNMENTS

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FILE REFERENCE: PH-1261-US
CURRENT APPLICATION NUMBER: US/09/938,901
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: JP2001-47762
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
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; TYPE: PRT
; ORGANISM: Thermus thermophilus
US-09-938-901-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-938-901-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           Query Match 99.8%; Score 1697; DB 10; Length 325; Best Local Similarity 99.7%; Pred. No. 2e-151; Matches 324; Conservative 1; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09938901 Publication No. US20030008291A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kuramitsu Seiki,
APPLICANT: Yokoyama Shigeyuki
TITLE OF INVENTION: GENE ENCODING DNA REPAIR ENZYME
                                           121 AFGERVAAVDGNVRRVLSRLFARESPKEKELFALAQGLLPEGVDPGVWNQALMELGATVC 180
181 LPKRPRCGACPLGAFCRGKEAPGRYPAPRKRRAKEERLVALVLLGRKGVHLERLEGRFQG 240
                                                                       121 AFGERVAAVDGNVRRVLSRLFARESPKEKELFALAQGLLPEGVDPGVWNQALMELGATVC 180
                                                                                                                                61 ALAAASLEEVLRVWQGAGYYRRAEHLHRLARSVEELPPSFAELRGLPGLGPYTAAAVASI 120
                                                                                                                                                            61 ALAAASLEEVLRVWQGAGYYRRAEHLHRLARSVEELPPSFAELRGLPGLGPYTAAAVASI 120
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ORGANISM: Homo sapiens
FEATURE:
INAME/KEY: SITE
LOCATION: (34)
OTHER INFORMATION: Xaa equals any of the naturally occurring
NAME/KEY: SITE
LOCATION: (438)
OTHER INFORMATION: Xaa equals any of the naturally occurring
NAME/KEY: SITE
LOCATION: (447)
OTHER INFORMATION: Xaa equals any of the naturally occurring
LOCATION: (447)
OTHER INFORMATION: Xaa equals any of the naturally occurring
OTHER INFORMATION: Xaa equals any of the naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and
FILE REFERENCE: PA106
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PAECHTIN Ver. 2.0
SEQ ID NO 1326
LENGTH: 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-09-925-301-1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1326, Application US/09925301
Patent No. US20020052308A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                    405
                                                                       234
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                                                                                                                                                                                                          164 DPGVWNQALMELGATVCLPKRPRCGACPLGAPCRGKE-----A
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                                                                                                                                                                                                                                                                                                                                                                                                                         106
                                                                                                                                                                                                                                                                                                                                                          55 RFFTLKALAAASLEEVLRVWQGAGYYRRAEHLHRLARS-VEEL---PPSFAEL--RGLPG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                            w
                        NSGLLAGLWEFPSVTWEPSEQLQRKALLQELQRXAGPLPATHXRHLGEVVHTPSHIKLTY 464
                                                          LEGRFQGLYGVP--LFPPEELPGREAAF------GVRSRPLGEVRHALTHRRLRV 280
EVRGALWEGE 290
                                                                                                                                     KWPTLQDLASASLEEVNQLWAGLGYYSRGRRLQEGARKVVEELGGHMPRTAETLQQLLPG
                                                                                                 PNTGQCHLCLPPSBPWDQTLGVVNFPRKASRKPPREESSATCVLEQPGALGAQILLVQRP
                                                                                                                                                                                                                                                                                            LGPYTAAAVASIAFGERVAAVDGNVRRVLSRLFA----RESPKEKELFALAQGLLPEGV 163
                                                                                                                                                                                                                                                                                                                                                                                                         AFRGSLLSWYDQEKRDLPWRRRAEDEMDLDRRAYAVWVSEVMLQQTQVATVINYYTGWMQ 165
                                                                                                                                                                                                                                                                                                                                                                                                                                              AWRKALLAWYRENARPLPWRG-----EKDPYRVLVSEVLLQQTRVEQALPYYRRFLE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLMEKVLRKALPLLAHAGVVPLPDA 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.4%; Score 483.5; DB 36.5%; Pred. No. 1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 106; Indels 83;
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Sequence 68280, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
ITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT FILING DATE: 203104-28

NUMBER OF SEQ ID NOS: 73128

EVALUATE: CAO. YOUR STEEL ST
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US-10-289-762-421
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US-10-289-762-421
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CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 421
LENGTH: 375
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 421, A Publication No.
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Griffais, R. TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
                                                                                       LENGTH: 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 KRRPKEMMAĞLYEFPYIEVEPEEĞLQDIEĞFTKKMELSLESPLEFLGNLKEQRHAFTNHK 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 LERLEGREQGLYGVPLFPPEELPGREAAFGVRSR-------PLGEVRHALTHRR 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 GATVCLPKRPRCGACPLGAFCRGKEAPGRYPAPRKRRAKE----ERLVALVLL-GRKGVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 LRV 280
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QVYGLALEGQ 474
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US-10-437-963-138271
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SEQ ID NO 138271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 138271, Application US/10437963 
Publication No. US20040123343A1
                                                                                                                                                                                                                                 Query Match
Best Local
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 474
TYPE: PRT
                                                                                                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT4530_39677C.1.pep
                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALMELGATVCLPKRPRCGACPLGAFC----RGKEAPGRYPAPR---KRRAKEERLVAL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAIASIAFNEVVPVVDGNVIRVISRLYTIADNPKESSTVKRFWDLVGQMVDPLRPGDFNQ 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVRSLAAATQEEVNEMWAGLGYYRRARFLLEGAKQIIEKGLFPCTALALREVRGIGDYTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLKALAAASLEEVLRVWQGAGYYRRAEHLHRLARSVEE---LPPSFAELRGLPGLGPYTÄ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALRAQLLRWYDAHRRDLPWRCVSGSEEERAYAVWVSEVMLQQTRVPVVVAYYERWMARWP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLLGRKGV------HLERL----EGRFQGLYGVPLFPPE----ELPGREAAFG- 260
  LPGLGPYTAAAVASIAFGERVAAVDGNVRRVLSRLFA-RESPKEKELFALAQGLLPEGVD
                                          YSRWMARWPTVDSLAAATQEEVNEMWAGLGYYRRARFILEGAKQIVEKGEFPCTASTLRE 175
                                                                                                                                                                   AWRKALLAWYRENARPLPWRGEKDP-----YRVLVSEVLLQQTRVEQALPY
                                                                                 YRRFLERFPTLKALAAASLEEVLRVWQGAGYYRRAEHLHRLARSV---EELPPSFAELRG 105
                                                                                                                              AVRAELLRWYDANRRDLPWRRAAEPPAGSGSGRGEEQRAYAVWVSEVMLQQTRVPVVVDY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barbazuk, Brad
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                                                                                                                                                                                                           Conservative
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35.0%;
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Pred. No. 2.3e-33;
4; Mismatches 113;
                                                                                                                                                                                                                                 Score 442; DB 16;
Pred. No. 8.3e-33;
                                                                                                                                                                                                                Mismatches 110;
                                                                                                                                                                                                                                                     DB 16;
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                                                                                                                                                                                                                                                     Length 474;
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; TYPE: PRT
; ORGANISM: E.
US-10-629-951-36
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  GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIRO
                                                                                                                                                    RESULT 7
US-10-156-761-12241
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PRIOR FILING DATE: 2000-07-31
PRIOR PPLICATION NUMBER: 09/463,891
PRIOR PILING DATE: 2000-01-28
PRIOR PILING DATE: 1090-01-28
PRIOR PILING DATE: 1998-07-28
PRIOR PILING DATE: 1998-07-28
PRIOR PPLICATION NUMBER: 60/053,936
PRIOR FILING DATE: 1997-07-28
PRIOR FILING DATE: 1997-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 36, Application US/10629951 Publication No. US20040018550A1 GENERAL INFORMATION:
                                                                                                     Sequence 12241, Application US/10156761
Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FE
SEQ ID NO 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 22.9%; Score 389.5; DB 15; Best Local Similarity 44.8%; Pred. No. 2.1e-28; Matches 81; Conservative 37; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bellacosa, Alfonso
TITLE OF INVENTION: Methods for Detection of Transition
TITLE OF INVENTION: Single-Nucleotide Polymorphisms
FILE REFERENCE: FCCC 96-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/629,951
CURRENT FILING DATE: 2003-07-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 PSRPGDFNQAMMELGATLCSKTKPGCSQCPVSSHCQALALSSQNASVKVTDFPRVVPKAK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 --- PGVWNQALMELGATVCLPKRPRCGACPLGAFCRGKEAPGR-----YP--APRKR 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 RAKEERLVALVLLGRKGVHLERLEGRFQGLYGVPLFPPEELPGREAAFGVRSRPLGEVRH 271
                                                                                                                                                                                                                                                                                196 C 196
                                                                                                                                                                                                                                                                                                                     122 AVSGWPGKKEVENKLWSLSEQVTPAVGVER--FNOAMMDLGAMICTRSKPKCSLCPLQNG 179
                                                                                                                                                                                                                                                                                                                                                             142 ARES-PKEKE----LFALAQGLLPE-GVDPGVWNQALMELGATVCLPKRPRCGACPLGAF 195
                                                                                                                                                                                                                                      180 C 180
                                                                                                                                                                                                                                                                                                                                                                                                          62 HKAAQQVATLHGGKFPETFEEVAALPGVGRSTAGAILSLSLGKHFPILDGNVKRVLARCY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 PYKVWLSEVMLQQTQVATVIPYFERFMARFPTVTDLANAPLDEVLHLWTGLGYYARARNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FastSEQ for Windows Version
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    IKEDA, HARUO
ISHIKAWA, JUN
HORIKAWA, HIROSHI
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Indels Length

121

61

188; 13;

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FILE REFERENCE: 249-125

CURRENT APPLICATION NUMBER: US/09/738,626

CURRENT FILING DATE: 2000-12-18

PRIOR APPLICATION NUMBER: JP 99/377484

PRIOR FILING DATE: 1999-12-16

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 7059

SOFTWARE: PATENTIN Ver. 3.0

SEQ ID NO 6433

TYPE: PRT
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
ITILE OP INVENTION: NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: UP 2001-272697
IPRIOR FILING DATE: 2001-08-02
IPRIOR APPLICATION NUMBER: UP 2001-272697
IPRIOR APPLICATION NUMBER: UP 2001-272697
IPRIOR APPLICATION NUMBER: UP 2001-272697
IPRIOR FILING DATE: 2001-08-02
IPRIOR APPLICATION NUMBER: UP 2001-272697
IPRIOR FILING DATE: 2001-08-02
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IPRIOR FILING DATE: 2001-08-02
IPRIOR FILING DATE: 2001-08-02
IPRIOR FILING DATE: 2001-08-02
IPRIOR FILING DATE: 2001-08-02
IPRIOR APPLICATION NUMBER: UP 2001-272697
IPRIOR FILING DATE: 2001-08-02
IPRIOR FILING DATE: 2001-0
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APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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US-09-738-626-6433
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APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: AIDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAKKO
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Publication No. US20020197605A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 DLÁKEAPGÉAVRÁWGRLGÝPRRÁLRLHGAÁVAITERHNGDVPTEHÁQLLALPGIGEÝTÁA 144
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Similarity 39.6%; Pred. No. 6.4e-27;
97; Conservative 32; Mismatches 88; Indels 2
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US-10-437-963-103808
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US-10-437-963-103808
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                                                                                                                                                                                                                               Query Match
Best Local 9
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SEQ ID NO 103808
LENGTH: 1719
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 103808, Application US/10437963 Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                    FEATURE:

NAME/KEY: unsure
LOCATION: (1)..(1719)

OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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Best Local Similarity
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105 GLPGLGPYTAAAVASIAFGERVAAVDGNVRRVLSRLFA-RESPKEKELFALAQGLLPEGV 163
                                                                                                                           54 AVRABILRWYDANRRDLPWRRAABPAGSGSGSGRGEEKRAYAVWVSEVMLQHTRVPVVVD 113
                                                                                                                                                                                                            105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 LIMDVLRNATAPVPLSAIDVVWPDDAQRSRALFSLIEDGLAEQNEA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 VHLERLEGRFQ--GLYGVPLFPPEELPGREAAFGVRSRPLGEVRHA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 ARÁVÁAFHÉGORÓPVÓDTNÓRKÓYOKAVÁGRYLAGÞAKKQELIDVSLÍLÍÐNTHAÐ-EFSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 AAAVASIAFGERVAAVDGNYRRYLSRLFARE---SPKEKELFALAQGLLPEGVDPGVWNQ 170
                                                                                                                                                                                                                         h 19.8%; Score 337;
Similarity 33.9%; Pred. No. 3.
                                                     YYSRWMARWPTVDSLÄÄÄTQEEVNEMWAGLGYYRRARFLLEGAKQIVEKGEFPRTASALR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 PEDFÁNÁSTDÉTÍRSWGKLGYFRRÁLRÍKECÁEVIVEKHAGÉVPDTVEALLAÍPGIGDYT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 LKALAAASLEEVIRVWQGAGYYRRAEHLHRLA----RSVEELPPSFAELRGLPGLGPYT 113
                                                                                       YYRRFLERFPTLKALAAASLEEVLRVWQGAGYYRRAEHLHRLARSV---EELPPSFAELR 104
                                                                                                                                                           AWRKALLAWYRENARPLPWR-------GEKDPYRVLVSEVLLQQTRVEQALP 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AWRKALLAMYRENARPLPWRGEKDP----YRVLVSEYLLQQTRVEQALPYYRRFLERFPT 58
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Barbazuk, Brad
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                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                        DB 16;
1.9e-22;
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                                                                                                                                                                                                       88;
                                                                                                                                                                                                                                       Length 1719;
                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                 Gaps
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Length

188; 11;

Gaps

139 60 84 4

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US-10-629-951-34
Sequence 34, Application US/10629951
Publication No. US20040018550A1
GENERAL INFORMATION:
APPLICANT: Bellacosa, Alfonso
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US-10-424-599-248081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 248081
LENGTH: 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 248081, Application US/10424599 Publication No. US20040031072A1
                                                                                                                                                 TITLE OF INVENTION: Methods for Detection of Transition TITLE OF INVENTION: Single-Nucleotide Polymorphisms FILE REFERENCE: FCCC 96-21
CURRENT APPLICATION NUMBER: US/10/629,951
CURRENT FILING DATE: 2003-07-29
PRIOR APPLICATION NUMBER: 09/463,891
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: PCT/US98/15828
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/053,936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                           PRIOR APPLICATION NUMBER: US/09/629,222A PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 WPTIHHLAQASLEEVNEMWAGLGYYRRARFLLEGAKKIVAEGGQIPKVASMLRNIPGIGE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                    182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 YTA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 PPTLKALAAASLEEVLRVWQGAGYYRRAEHLHRLARSV----EELPPSFAELRGLPGLGP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 RVALLDWYDLNRRDLPWRTTFKQEDEEVERRAYGVWVSEVMLQQTRVQTVIAYYNRWMQK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RKALLAWYRENARPLPWRG-----EKDPYRVLVSEVLLOOTRVEQALPYYRRFLER 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAARLAAAELAAARAEAEAAEDAARAAEVEVETLRSSINGSIAGDITADREL--EELA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEERLVALVLLGRKG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGVRSRPLGE 268
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Pred. No. 1.6e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12; Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35;
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NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7283, Application US/10335977

Publication No. US20040052799A1

GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 188
TYPE: PRT
ORGANISM: M.
                                                                                                                                   INFORMATION FOR SEQ ID NO: 7283:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/993,002

PRIOR APPLICATION NUMBER: 08/993,002

PRIOR APPLICATION NUMBER: 08/993,002

PRIOR DATE: 17-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Mandaragounas, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: GTN-018

TELECHONE: (617)227-7400

TELECHONE: (617)227-7400

TELECHAR: (617)742-4214

TELECAR: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
                        TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 10031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 C 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 LFARE----SPKEKELFALAQGLLPEGVDPGVWNQALMELGATVCLPKRPRCGACPLGAF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 QLKELARVVINDYGGRVPRNRKAILDLÞGVGKYTCAAVMCLAFGKKAAMVDANFVRVINR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 HLHRLARSY-----EELPPSFAELRGLPGLGPYTAAAVASIAFGERVAAVDGNVRRVLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 DPYRVLVSEVLLQQTRVEQALPYYRRFLERFPTLKALAAASLEEVLRVWQGAGY-YRRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DPYVILITEILLRRTTAGHVKKIYDKFFVKYKCFEDILKTPKSEIAKDIKEIGLSNORAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: WINDOWS NT SOFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
                                                                                           TYPE: amino acid
                                                                                                                    LENGTH: 230 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/335,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thermoformicicum
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                                                                                                                                                                                                                                                   GTN-018
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Matches

Gaps

62

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RESULT 13
US-10-335-977-7282
J. Sequence 7282, Application US/10335977
Publication No. US2004052739A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION NUCLEIC ACID AND AMINO ACID SEQUENCES
DIAGNOSTICS AND THERAPEUTICS
                                                               INFORMATION FOR SEQ ID NO: 7282:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ' NAME/KEY: misc_feature ' LOCATION: (B) LOCATION 1...230 ' SEQUENCE DESCRIPTION: SEQ ID NO: 7283: US-10-335-977-7283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEc-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELEPHONE: (617)27-7400
TELEPHONE: (617)27-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 NLEFKLPF-----LGTIKHSHTKFKLNLNL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 --PEELPGREAAFGVRSRPLGEVRHALTHRRLRVEV 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 FCRGKEAPGRYPAPRKRR-AKEERLVALVLLGRKGVHLERLEGRFQGLY-GVPLFP---- 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 AQGLLPEGVDPGV------WNQALMELGATVCLPKRPRCGACPLGA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 -----ĠĿĎĖNIHAKDLQIKANDFLNLNESFNHŇQĀĹIDĹĠÁLIĊSĖK-ĖKĊAIĊĖFNP 105
                                       ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 ELPPSFAELRGLPGLGPYTAAAVASIAFGERVAAVDGNVRRVLSRLFARESPKEKELFAL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 QĽPNDYQSĽLKĹPĠIĠAŸŤÁNÀILCFGFREKSÁCVĎAŇÝKŔVĽLŘĹF-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YĊĿĠŔŊĦĿŖĦŦĿĸĸŔQEIIQĖĖĸYĿĠVŸIQNNQ-ĪAĿĖĸĪĖ---ŎĸĹŶĿĠŊĦĦĖĎŊĿĸE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                             (617) 742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.8%;
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Pred. No. 1.3e-13;
2; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 230;
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Query Match
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Publication No. US20040052799A1

GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPBUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...187; SEQUENCE DESCRIPTION: SEQ ID NO: 7282: US-10-335-977-7282
                                                                                                                                                                                                                               TELEPHONE: (617)227-7400
INFORMATION FOR SEG ID NO: 7279:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                    NAME/KEY: misc feature LOCATION: (B) LOCATION 1...98
SEQUENCE DESCRIPTION: SEQ ID NO: 7279:
                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL; YES ORIGINAL SOURCE:
                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                          NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207 REFERENCE/DOCKET NUMBER: GTN TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 YCLGKNHLERHTLKKKQEIIQEERYLGVVIQNNQ-IALEKIB---QKLYLGMHHFP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 FCRGKEAPGRYPAPRKRR-AKEERLVALVLLGRKGVHLERLEGRFQGLY-GVPLFP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 AQGLLPEGVDPGV-----------WNQALMELGATVCLPKRPRCGACPLGA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 -----ĠLDŶNIHAKDLQIKANDFLNLNESFNHNQĀĹIDĹĠĀLIĊSÞK-ÞKĊAIĊÞFNP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 QLÉNDYQSÍLKÍÞÍGIGAÝTÁNÁILCFGFRÉKSÁCVDANVKRVÍLRÍF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 ELPPSFAELRGLPGLGPYTAAAVASIAFGERVAAVDGNVRRVLSRLFARESPKEKELFAL 154
                                                                                                                ORGANISM: Helicobacter pylori
                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                  GTN-018
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11.8%;

Score 200.5;

DB 12;

Length

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US-10-335-977-7280
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LOCATION: (B) LOCATION 1...98
SEQUENCE DESCRIPTION: SEQ ID NO: 7280:
US-10-335-977-7280
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Sequence 7280, Application US/10335977

Publication No. US20040052799A1

GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity Matches 45; Conserv
                                                                                                                                                               Matches
                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 7280:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION UNDEER: 08/993,002
APPLICATION NUMBER: 08/993,002
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 FPTLKDLANAPLEEVLLLWRGLGYYSRAKNLKK 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 FPTLKALAAASLEEVLRVWQGAGYYRRAEHLHR 88
61
                                      56
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                                                                                                                                                               45;
                                                                                                     1 MEAWRKALLAWYRENAR-PLPWR---GEKDPYRVLVSEVLLQQTRVEQALP-YYRRFLER 55
                                                                             1 LETLHNALLKWYEEFGRKDLPFRNLKGINAPYEVYISEVMSQQTQISTVIERFYPPFLKA 60
                            FPTLKALAAASLEEVLRVWQGAGYYRRAEHLHR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
PPTLKDLANAPLEEVILLWRGLGYYSRAKNIKK 93
                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                             11.8%; Score 200.5; DB 12; llarity 48.4%; Pred. No. 6e-11; Conservative 14; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.4%;
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                                                                                                                                                                                                      Length 98;
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Search completed: October 6, 2004, 20:29:46
Job time : 133 secs

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MEAWRKALLAWYRENARPLP.....VLRKALPLLAHAGVVPLPDA 325
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1701
1 Issued_Patents AA:*
2: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/CTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	ø	œ	7	თ	ຫ	4.	w	N	_	Result No.
164.5	164.5	164.5	171	172	176	176	188	191	240.5	274.5	274.5	274.5	355	389.5	442	443	450	457.5	471.5	471.5	471.5	477	477.5	481.5	485	505	Score
9.7	9.7	9.7	10.1	10.1	10.3	10.3	11.1	11.2	14.1	16.1	16.1	16.1	20.9	•				26.9	•	27.7	27.7	28.0	•		28.5	29.7	Query Match Length
304	297	211	204	209	259	207	227	185	188	225	221	221	414	188	346	360	347	516	350	350	350	375	470	535	395	403	1
2	N	N	N	N	N	N	4	4.	4.	4	4	_	4	Α.	4	4	4	4.	4	4	w	4	4	w	4.	4	DB
US-08-808-550-2	US-08-808-550-42	US-08-808-550-37	US-08-808-550-32	8-550-3	US-08-808-550-39	US-08-808-550-36	US-09-107-532A-3843	US-09-629-222A-35	US-09-629-222A-34	US-10-037-927B-14	US-09-402-959A-10	US-08-663-023-17	US-09-540-236-2578	US-09-629-222A-36	US-09-328-352-4982	US-09-134-001C-4684	US-09-543-681A-5315	US-09-489-039A-11959	US-09-650-855-37	US-09-651-656-37	US-08-813-574-9	US-09-198-452A-421	US-09-252-991A-23310	-574-2	US-09-134-000C-5115	US-09-107-532A-7308	ID
Sequence 2, Appli	42,	Sequence 37, Appl		31,	39,	36,	384	35, Ar	34,	Sequence 14, Appl	10,	17,	2578	36,	4982	4684	æ	1195	37,	e 37,	9, 1	e 421	23	e 2, Apr	e 5115,	Sequence 7308, Ap	Description

4 5	44	43	42	41	40	39	38	37	36	35	34	ω u	32	31	30	29	83
115	115.5	117	118.5	121	121	127.5	128	134	137.5	142	145	145	145	145	154	158	160
6. 8	6.8	6.9	7.0	7.1	7.1	7.5	7.5	7.9	8.1		5	8. 5	8 5	8 .5	9.1	9.3	9.4
542	494	230	776	4472	216	212	628	207	184	216	211	211	211	207	213	185	477
4	4	4.	4	N	4	4.	4	N	4.	4	4	4,	ผ	2	N	4.	æ
US-09-252-991A-21753	US-09-252-991A-17295	US-09-328-352-5770	US-09-252-991A-28446	US-08-804-227C-2	US-09-543-681A-4806	US-09-252-991A-17572	US-09-252-991A-30904	US-08-808-550-30	US-09-629-222A-33	US-09-489-039A-9560	US-09-650-855-25	US-09-651-656-25	US-08-808-550-38	US-08-808-550-29	US-08-808-550-35	US-09-134-000C-3440	09-03-104-001C-060
Sequence	Sequence	Sequence			Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence				Sequence	ocductice
21753, A	17295, A	5770, AD		z, Appli	4806, Ap	17572, A	30904, A	30, App1	33, Appi		25, Appi	•	Je, Appi	rddw '67	35, Appl	3440, Ap	C

ALIGNMENTS

RESULT 1 US-09-107-532A-7308 Sequence 7308, Application US/09107532A Sequence 7308, Application US/09107532A Patent No. 6593275 GENERAL INFORMATION: APPLICANY: Lynn A DOUCETC SCID AND ANINO ACID SEQUENCES RELATING TO THILD OF INVENTION: APPLICANY: 1910 CORRESPONDENCE ADDRESS: ADDRESSES: ADDRESS: ADDRESSES: GENOME THERAPEUTICS CORPORATION STREET, 100 Beaver Street STATE: Massachusetts COUNTR: USA ZIP: 03254 COMPUTER READABLE FORM: SDETWARE: ASCII I CORPUTER READABLE FORM: SOFWARE: ASCII SOFWARE: ASCII CORPORATION PRILING DATE: 14 May 1998 APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 AREFERENCE/DOCKET WUMBER: CTC-012 TELEPONE: (781)99-8277 INFORMATION FOR SEQ ID NO: 7308: SEQUENCE CHARACTERISTICS: LENGTH: 403 maino acids TODOLOCY: 11 mear DOCATION: (B) LOCATION BESTURE: 14 May 1998 ANDLE LIN TELEPON: (781)99-8277 INFORMATION OCID TELEPON: (781)99-8277 INFORMATION OCID THERE AND ACID ORANISM: ENERGENCE CHARACTERISTICS: SOURCE: TYPE: pamino acids TODOLOCY: 11 mear DOCATION: (B) LOCATION DOCATION IN COLUMN DOCATION I
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US-09-134-000C-5115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
US-09-134-000C-5115
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5115, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR FAPLICATION NUMBER: US 60/055,778
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
LENGTUP. 106

SEQ ID NO 5115
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                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local
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                                                                                                                                                                                                                                                                                            Matches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 29.7
Best Local Similarity 32.7
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                             Local Similarity
                                                     165
                                                                                                 109 LGPYTAAAVASIAFGERVAAVDGNYRRVLSRLFARES----PKEKELFALAQGLLPEGVD 164
                                                                                      129
                                                                                                                                                          69
                                                                                                                                                                       54 EREPTLKALAAASLEEVLRVWQQAGYYRRAEHLHRLARSV----EELPPSFAELRGLPG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 V 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307 L 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 RSRPLGEVRHALTHRRLRVEV-RGALWEGEGED------PWKRP------LPKLMEKV 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 RDSQKLLANMWTFPMMEVTQEEYERLKKEWETKPEIDLFDDLVAEEEQNLPFEKQELFVW 329
                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                           2 EAWRKA-----LIAWYRENARPIPWRGEKDPYRVLVSEVLLQQTRVEQALPYYRRFL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 ERVAAVDGNVRRVLSRLFARES----PKEKELFALAQGLLPEGVDPGVWNQALMELGATV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 KLĹKAWEĞLĞYYSKARNIQAAAKQIMSEFDGEMPQTPEEISSLKĞIĞPYTTGAIASİAFĞ
                PGVWNQALMELGATVCLPKRPRCGACPLGAFCRGKEAP--GRYPAPRKR-RAKEERLVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32
                                                                   IGPYTAGAIGSIAFNLREPAIDGNVMRVVSRLFEIDADIAKASSRKVFEAANLKIIDRER 188
                                                                                                                                       QTRHLGEVTHIFSHLKWHVLLFYGRATEGAEQEFTENKTSKWLKFDAFDSVVFFKVQMKL 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLPKRPRCGACPLGAFC----RGKEAPGRYPA-PRKRRAKEERLVALVLLGRKGVH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTPTSPKCETCPIQAPCLANKRGIQT--SFPVKTKKAKPKDVYYISAALQNHSGAYYFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPEPÁVDGNVMRVVSŘÍFCIBADIAKASSRKIFDBAMRKIIDEKHPĞBENQAMMDLĞSAI 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVLRVWQGAGYYRRAEHLHRLARSV-----EELPPSFAELRGLPGLGPYTAAAVASIAFG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQWYEQEKRNI.PWRYNRDPYRIWISEIMIQQTRVDTVIDYFYRFMEWFFTIEELANAPEE
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                         28.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.7%; Score 505; DB 4; Length 40: 32.7%; Pred. No. 1.8e-42; tive 66; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                       56;
                                                                                                                                                                                                                                                                                 Score 485; DB 4; Lo
Pred. No. 1.8e-40;
6; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 403;
                                                                                                                                                                                                                                                                                                                Length 395;
                                                                                                                                                                                                                                                                                 Indels 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64;
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                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-813-574-2
                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
US-08-813-574-2
(Sequence 2, Application US/08813574)
(Patent No. 6013473)
                                                                                                                                                                                                                                                             Ouery Match 28.3%; Score 481.5; DB 3 Best Local Similarity 36.5%; Pred. No. 6.2e-40; Matches 135; Conservative 46; Mismatches 106
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/813,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 05/06/813,57
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMER: 60/013,132
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG5000:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEPHAX: 610-270-4026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Wei, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 709 Swedeland CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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164 DPGVWNQALMELGATVCLPKRPRCGACPLGAFCRGKE-----
                                                                                                                     141 KWPTLQDLASASLEEVNQLWAGLGYYSRGRRLQEGARKVVEELGGHMPRTAETLQQLLPG
                                                                201
                                                                                                 109
                                                                                                                                                 55 RFPTLKALAAASLEEVLRVWQQAGYYRRAEHLHRLARS-VEEL---PPSFAEL--RGLPG 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 IIENKKQEFL--LEQRPETGLLANMWLFPIEEISKKQFQQLQKLAQPAETEKQLTLELEP 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 VLLGRKGVHLERLEGRFQG--LYGVPLFPPEELPGRE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 PGDFNQALMDLGSAVCTPTSPKCESCPLQQYCAAYQADKMTAYPVKSKKVKPKDVYYVGT
                                               VGRYTAGÁTÁSTÁFGQATGVVDGNVARVÍLCRVRÁTGADPSSTLVSQQLWGLÁQQLV-DPA 259
                                                                                LGPYTAAAVASIAFGERVAAVDGNVRRVLSRLFA----RESPKEKELFALAQGLLPEGV 163
                                                                                                                                                                                     PA
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                                                                                                                                                                                                                                                                                              DB 3;
                                                                                                                                                                                                                                                               106;
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RESULT 5
US-09-198-452A-421
; Sequence 421, Application US/091:
; Sequence 421, Application US/091:
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICAUN: GETIÉTAIS, R.
; APPLICAUN: GETIÉTAIS, R.
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US-09-252-991A-23310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 23310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23310, Application US/09252991A Patent No. 6551795
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Best Local
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALAAASLEEVLRVWQGAGYYRRAEHLHRLA----RSVEELPPSFAELRGLPGLGPYTAA 115
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                                                                                                                                                                                                                                                                                                                                                                               AIASLSMGLRAPILDGNVKRVLARYLAQDGYPGEPKVARALWEAAERFTPH-ARVNHYTQ
                                                                                                                                                                                                                                                                                                                                                                                                             AVASIAFGERVAAVDGNVRRVLSRLFARE----SPK-EKELFALAQGLLPEGVDPGVWNQ 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGFNGAVLDWYDRHGRKDLPWQQGITPYRVWVSEIMLQQTQVSTVLGYFDRFMAALPDVE 178
                                                                                                                                                            QLAIEPWLVAVEGAPRAVAEGDWLWYNLATPP-RLGLAAPVKKLLKRA
                                                                                                                                                                                                  RLRVE-----VRGA------LWEGEGEDPWKRPLPKLMEKVLRKA 310
                                                                                                                                                                                                                                   RDGAILLYRRPSSGLWGGLWSLPEL--DDLDGLEPLAARHSLALGERRELSGLTHTFSHF
                                                                                                                                                                                                                                                                     RKG---VHLERLEGRFOGLYGVPLFPPEELPGREAAFGVRSRPLGEVR-----HALTHR 276
                                                                                                                                                                                                                                                                                                        AMMDLGATLCTRSKPSCLLCPLVSGCRAHLLGREAD - - YPQPKPRKALPQKRTLMPILAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALAAAAEDEVLHLWTGLGYYSRARNLHKTAQIVVERHAGEFPRDVEQLAELPGIGRSTAG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.1%; Score 477.5; DB 4; 36.2%; Pred. No. 1.3e-39; vative 58; Mismatches 119;
                                                                        US/09198452A
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   genomic sequence and polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 470;
                                                                                                                                                                  460
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   fragments
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US-08-813-574-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 421
LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application Patent No. 6013473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: thereof and uses thereof, in particular TITLE OF INVENTION: and treatment of infection FILE REFERENCE: 9710-003-999 CURRENT APPLICATION NUMBER: US/09/198,452A CURRENT FILING DATE: 1998-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
           CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/013
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,3,
REFERENCE/DOCKET NUMBER: 34,3,
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wei, Ying-Fei
TITLE OF INVENTION: Human
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Be
STREET: 709 Swedeland Ro
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Chlamydia pneumoniae
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                                                                                                                                                                                                                                                              ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/813,574
TELECOMMUNICATION
                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                              COMPUTER: IBM CO
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 SLEEVLRVWQGAGYYRRAEHLHRLARSVEE-----LPPSFAELRGLPGLGPYTAAAVASI
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                                                                                                                                                                                                                                               IBM Compatible
                                                                                                                                                                                                                                                                   Diskette
 INFORMATION
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                    ATG50002
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Pred. No. 1.1e-39;
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TITLE OF INVENTION: DETECTION AND QUANTITAT
TITLE OF INVENTION: POLYMORPHISMS, DNA SEQU
TITLE OF INVENTION: DOLYMORPHISMS, DNA SEQU
FILE REFERENCE: IL-10689
CURRENT APPLICATION NUMBER: US/09/651,656
CURRENT FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: 60/192,764
PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 37
LENGTH: 350
TYPE: PAT
ORGANISM: Escherichia coli
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US-09-651-656-37
Sequence 37, Application US/09651656
Patent No. 6340566
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MCCUTHEN-MALONEY, SANDRA
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
TITLE OF INVENTION: DETECTION AND QUANTITATION OF SINGLE NUCLEOTIDE
TITLE OF INVENTION: POLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTATIONS,
TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 121;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TENGTH: 350 amino acids
TYPE: amino acid
STRANUEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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TELEFAX: 610-270-4026
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67 LEEVLRVWQGAGYYRRAEHLHRLARSVEEL-----PPSFAELRGLPGLGPYTAAAVASIA 121
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                                                         8 LLAWYRENAR-PLPWRGEKDPYRVLVSEVLLQQTRVEQALPYYRRFLERFPTLKALAAAS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 FGERVAAVDGNVRRVLSRLFARES-PKEKE----LFALAQGLLPE-GVDPGVWNQALMEL 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 LDEVLHLWTGLGYYARARNLHKAAQQVATLHGGKFPETFBEVAALPGVGRSTAGAILSLS 129
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                                                                                                                                          Similarity
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                                   VLDWYDKYGRKTLPWQIDKTPYKVWLSEVMLQQTQVATVIPYFERFMARFPTVTDLANAP 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.7%; Score 471.5; DB 3; ilarity 35.1%; Pred. No. 3.5e-39; Conservative 61; Mismatches 120;
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APPLICANT: MCCUTHEN-MALONEY, SANDRA
APPLICANT: MCCUTHEN-MALONEY, SANDRA
APPLICANT: MCCUTHEN-MALONEY
TITLE OF INVENTION: CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA
TITLE OF INVENTION: MISMATCHES
TITLE OF INVENTION: MISMATCHES
FILE REFERENCE: IL-10284
CURRENT APPLICATION NUMBER: US/09/650,855
CURRENT PILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: 60/192,764
PRIOR APPLICATION NUMBER: 60/192,764
PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 37
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Patent No. 6365355
GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mac
Local 5
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                                                                                                                                                                                                                    176 GATVCLPKRPRCGACPL--GAFCRGKEAPGRYPAPRKRRAKEERLVALVLLGRKGVHL--
                                                                                                                                                                                                                                                         130 LGKHFPILDGNVKRVLARCYAVSGWPGKKEVENKLWSLSEQVTPAVGVER--FNQAMMDL
                                                                                                                                                                                                                                                                            122 FGERVAAVDGNVRRVLSRLFARES-PKEKE----LFALAQGLLPE-GVDPGVWNQALMEL 175
                                                                                                                                                                                                                                                                                                                                                              67 LEEVIRVWQGAGYYRRAEHIHRLARSVEEL-----PPSFAELRGLPGLGPYTAAAVASIA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 GAMICTRSKĖKOSLOPLQNGCIAAANNSWALYPGKKPKQTLPERTGYFLLLQHEDEVLLA
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                                            PVSSFTGCMDEGNALWYNLAQPPSVGLAAPVERLLQQ-LRTGAPV
                                                                            -----EVRGALWEGEGEDP---WKRPLPKLMEKVLRKALPL 313
                                                                                                             QRPPSGLWGGLYCFPQFADEESLRQWLAQRQIAADNLTQ-LTAFRHTFSHFHLDIVPMWL
                                                                                                                                                 -ERLEGRFQGLYGVPLFPPEE-----LPGREAAFGVRSRPLGEVRHALTHRRLRV----
                                                                                                                                                                                    GAMICTRSKĖKOSLOPLONGCIAAANNSWALYPGKKPKOTLPERTGYFLLLQHEDBVLLA
                                                                                                                                                                                                                                                                                                                              LDEVLHLWTGLGYYARARNLHKAAQQVATLHGGKFPETFEEVAALPGVGRSTAGAILSLS 129
                                                                                                                                                                                                                                                                                                                                                                                                   VLDWYDKYGRKTLPWQIDKTPYKVWLSEVMLQQTQVATVIPYFERFMARFPTVTDLANAP 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----EVRGALWEGEGEDP---WKRPLPKLMEKVLRKALPL 313
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APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACITITLE OF INVENTION: DIAGNOSTICS AND THERAPEU
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5315
LENGTH: 347
TYPE: DET
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11959
LENGTH: 516
TYPE: PRT
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Best Local :
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APPLICANT: Gary Br
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                                                                Query Match
                                    Matches
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                                                                                                             TYPE: PRT
ORGANISM: Proteus mirabilis
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                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGOHYPILDGNVKRVLARCYAVSGWPGKKEVEKRLWDISEEVTPAEGVER--FNQAMMDL 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEEVLRVWQGAGYYRRAEHLHRLARSVE-----ELPPSFAELRGLPGLGPYTAAAVASIA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLDWYDKYGRKTLPWQIAKTPYKVWLSEVMLQQTQVTTVIPYFERFMARPPTVVDLANAP 235
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EAWRKALLAWYRENAR-PLPWRGEKDPYRVLVSEVLLQQTRVEQALPYYRRFLERFPTLK 60
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                                                26.5%; Score 450; DB 4; 33.2%; Pred. No. 5e-37;
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; Pred. No. 1.5e-37;
63; Mismatches 119;
                                  64;
                                                                                                                                                                                                                                                                                    AND AMINO ACID SEQUENCES AND THERAPEUTICS
                                  Mismatches
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                                                                  Length 347;
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     RESULT 12
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RESULT 11
US-09-134-001C-4684
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APPLICATI: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4684
LENGTH: 360
TYPE: NEW TOWN THE TOWN THE THE TOWN THE 
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                                                                                                                      --ERLEGREQGLYGVPLEPPEELPGREA-----AFGVRSRPLGEVRHALTHRRLRVEV
LEKRKEKLLNGMWQFPM--REQTNANDVISDDLGKSIETINEPVFKLKHQFTHLTWEIKV
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RESULT 13
US-09-629-222A-36

Sequence 36, Application US/09629222A

Patent No. 6599700

GENERAL INFORMATION:
APPLICANT: Bellacosa, Alfonso
ITILE OF INVENTION: Methods for Detection of Transition
ITILE OF INVENTION: Single-Nucleotide Polymorphisns
CURRENT APPLICATION NUMBER: US/09/629,222A

CURRENT FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 09/463,891
PRIOR APPLICATION NUMBER: PCT/US98/15828
PRIOR APPLICATION NUMBER: PCT/US98/15828
PRIOR APPLICATION NUMBER: 60/053,936
PRIOR FILING DATE: 1998-07-28

NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 3.0

LENTTH: 188
Query Match
Best Local Similarity 44.0
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; Patent No. 6562958
; GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER FILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; SEQ ID NO 4982
; LENCTH: 346
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4982
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                                                                                             -09-629-222A-36
                                                                                                       LENGTH: 188
TYPE: PRT
ORGANISM: E.
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Similarity 33.3%;
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               22.9%; Score 389.5; DB 4;
44.8%; Pred. No. 2.6e-31;
ative 37; Mismatches 50;
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Pred. No. 3.2e-36;
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                                               DB 4;
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                 Indels
                                               Length 188;
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RESULT 15
US-08-663-023-17
; Sequence 17, Application US/08663023
; Patent No. 5763178
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US-09-540-236-2578
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Patent NO. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2578
LENGTH: 414
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Matches 109;
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ORGANISM: M.catarrhalis
                                                                                      389
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                                                                                LWT---DTPYNLPLPAAMHKLL 407
                                                                                                              LWEGEGEDPWKRPLPKLMEKVL
                                                                                                                                   HDLLHSQLIEILPIPTQTLTAYLRHTLTHVHWHLYGMSICLNNSQFNQINQTLTGLGIDY
                                                                                                                                                                     FGVRSRPLGEV-----RHALTH-----
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                                                                                                                                                                                                                           LLG---RKGVHLERLEGRFQGLYGVPLFPPEELP-----
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                                                                                                                                                                                                                                                                                                               RSTĀGĀIVAMGVKKFGVICDGNVKRVLARHRĀVCGDITKSATDKRLWEIĀTALTPKEYS- 211
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                                                                                                                                                                                                                                                                                                                                                                       TVQEĽAVADWQEVASFWAĞLĞYYAKARNLHAGAQQVADFIDTHGRFPETVNEWQAVKĞVĞ 152
                                                                                                                                                                                                                                                                                                                                                                                                  TLKALAAASLEEVLRVWQQAGYYRRAEHLHRLARSYEE-----LPPSFAELRGLPGLG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                SFAKRLLTWFELHGRHGLPWQYHHQPSADIYAVWVSEIMLQQTQVVTVLKFFEPFLARPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVSGWPGKKEVENKLMSLSEQVTPAVGVER--FNOAMMDLGAMICTRSKPKCSLCPLQNG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARES-PKEKE----LFALAGGLLPE-GVDPGVWNQALMELGATVCLPKRPRCGACPLGAF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HKAAQQVATLHGGKFPETFEEVAALPGVGRSTAGAILSLSLGKHFPILDGNVKRVLARCY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HRLARSVEEL-----PPSFAELRGLPGLGPYTAAAVASIAFGERVAAVDGNVRRVLSRLF 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYKVMLSEVMLQQTQVATVIPYFERFMARFPTVTDLANAPLDEVLHLWTGLGYYARARNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.9%; Score 355; DB 4; I
28.5%; Pred. No. 2.3e-27;
tive 57; Mismatches 132;
                                                                                                              307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 414;
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                                                                                                                                                                 ---RRLRVEVRGA----
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TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-663-023-17
Search completed: October 6, 2004, 20:19:07 Job time : 21 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 16.1%; Score 274.5; DB 1; Length 221; Best Local Similarity 31.7%; Pred. No. 1.2e-19; Matches 63; Conservative 40; Mismatches 85; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION UMBER: US/08/663,023
PILING DATE: 07-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,950
APPLICATION NUMBER: US 60/012,950
APPLICATION NUMBER: US 60/012,950
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,089
PILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/483,089
PILING DATE: 07-JUN-1995
APPLICATION NUMBER: 29.768
REFERENCE/DOCKET NUMBER: 66669/110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: CHIRIKJIAN, Jack G.
APPLICANT: CHILIER, G. Bruce
APPLICANT: COLLLER, G. Bruce
TITLE OF INVENTION: OSCILLATING SIGNAL AMPLIFIER FOR NUCLEIC
TITLE OF INVENTION: ACID DETECTION
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 904136
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 221 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                   178
                                                                                                                                                                                                     136 FGKKAAMVDANFVRVINRYFGGSYENLNYNHKALWELAETLVPGGKCRD-FNLGLMDFSA 194
                                                                                                                                                                                                                                                   122 FGERVAAVDGNVRRVLSRLFARE----SPKEKELFALAQGLLPEGVDPGVWNQALMELGA 177
                                                                                                  195 IIĆAPRKPKĆEKĆGMSKLĆ 213
                                                                                                                                                                                                                                                                                                        76 SETAKDIKEIĞLSNORAEQLKELARVVINDYGGRVPRNRKAILDLPGVGKYTCAAVMCLA 135
                                                                                                                                                                                                                                                                                                                                                      68 EEVLRVWQGAGY-YRRAEHLHRLARSY-----EELPPSFAELRGLPGLGPYTAAAVASIA 121
                                                                                                                                                                                                                                                                                                                                                                                                           16 ILTEWNTDRRDFFWRHTRDPYVILITEILLRRTTAGHVKKIYDKFFVKYKCFEDILKTFK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 LLAWYRENARPLPWRGEKDPYRVLVSEVLLQQTRVEQALPYYRRFLERFPTLKALAAASL 67
                                                                                                                                             TVCLPKRPRCGACPLGAFC 196
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (202) 672-5399
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Title:
Perfect score:
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9:
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112.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications NA:*

1: /cgn2 6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2 6/ptodata/2/pubpna/US06 NEW PUB.seq:*

3: /cgn2 6/ptodata/2/pubpna/US06 NEW PUB.seq:*

4: /cgn2 6/ptodata/2/pubpna/US07 NEW PUB.seq:*

5: /cgn2 6/ptodata/2/pubpna/US07 NEW PUB.seq:*

6: /cgn2 6/ptodata/2/pubpna/US07 NEW PUB.seq:*

8: /cgn2 6/ptodata/2/pubpna/US08 PUBCOMB.seq:*

9: /cgn2 6/ptodata/2/pubpna/US08 PUBCOMB.seq:*

10: /cgn2 6/ptodata/2/pubpna/US09 PUBCOMB.seq:*

11: /cgn2 6/ptodata/2/pubpna/US09 PUBCOMB.seq:*

12: /cgn2 6/ptodata/2/pubpna/US09 PUBCOMB.seq:*

13: /cgn2 6/ptodata/2/pubpna/US09 NEW PUB.seq:*

14: /cgn2 6/ptodata/2/pubpna/US09 NEW PUB.seq:*

15: /cgn2 6/ptodata/2/pubpna/US09 NEW PUB.seq:*

16: /cgn2 6/ptodata/2/pubpna/US10B PUBCOMB.seq:*

16: /cgn2 6/ptodata/2/pubpna/US10B PUBCOMB.seq:*

17: /cgn2 6/ptodata/2/pubpna/US10B PUBCOMB.seq:*

18: /cgn2 6/ptodata/2/pubpna/US10B PUBCOMB.seq:*

19: /cgn2 6/ptodata/2/pubpna/US10B PUBCOMB.seq:*
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Match Length DB
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                 10 US-09-938-901-1
15 US-10-156-761-4691
17 US-10-469-992-9
19 US-09-974-300-1583
17 US-10-437-963-1325
13 US-10-425-114-32132
15 US-10-216-817-21
15 US-10-216-817-21
17 US-10-437-963-35788
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Sequence 1, Appli
Sequence 46, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 1583, Ap
Sequence 1583, Ap
Sequence 32132, Ap
Sequence 32132, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
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Sequence 1,

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122 Q Q	watch ocal s g 974 2	15 71.4 7.3 930 11 16 68.2 7.0 991 11 18 68.2 7.0 991 11 18 68.2 7.0 3155 11 20 66.8 6.9 18976 11 20 66.8 6.9 18976 11 21 66.8 6.9 18976 11 22 64.6 6.6 1230 11 22 64.6 6.6 1230 11 23 63.8 6.5 47988 11 24 63.8 6.5 47988 11 25 63.6 6.2 6.4 15120 11 29 62.2 6.4 15120 11 20 10 10 11 20 10 10 11 20 10 10 10 11 20 10 10 10 11 20 10 10 10 11 20 10 10 10 11 20 10 10 10 10 10 10 10 10 10 10 10 10 10
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BAGAAGG BAGAAGG BAGGCCC	99. 100 Ervative TGGCGGA	930 15 1 930 15 1 931 16 1 11058 15 1 11876 15 1 1230 15 1 1230 15 1 1232 16 1 1237 16 1 1237 16 1 1237 16 1 1237 16 1 1348 17 1 1484 17 1 1484 17 1 1484 17 1 1484 17 1 1484 17 1 1484 17 1 1484 17 1 1484 17 1 1484 17 1 1484 17 1 1484 17 1 1484 17 1 1484 17 1 1484 17 1 1484 17 1 1484 17 1 1484 17 1 1484 17 1 1484 17 1 1566 13 1 2036 15 15 15 15 15 15 15 15 15 15 15 15 15
ACCC	9%; .0%; AAGC	8 15 US 16 US 16 US 15 US 15 US 15 US 16 US 16 US 17 US 9 17 US 9 17 US 17 US 17 US 17 US 17 US 17 US 18 US 19 US 10 US 11 US 11 US 11 US 1291A1 13 US 13 US 13 US 14 US 15 US 17 US 18 US 19 US 10 US 11 US 11 US 11 US 12 US 13 US 14 US 15 US 16 US 17 US 18 US 19 US 10 US 11 US 11 US 11 US 11 US 12 US 13 US 14 US 15 US 16 US 17 US 18 US 19 US 10 US 11 US 11 US 11 US 11 US 11 US 11 US 1291A1 13 US 14 US 16 US 17 US 18 US 19 US 10 US 11 US 1291A1 11 US 1291A1 11 US 11 US 1291A1 11 US 1291A1 11 US 1291A1 11 US 1291A1 11 US 1291A1 11 US 1291A1 11 US 1291A1 11 US 1291A1 1291A1 13 US 13 US 13 US 14 US 15 US 16 US 17 US 18 US 19 US 19 US 10 U
GGCGGGGGAGAAGAACCCTTACCGCGTCCTGGTCTCCGAGGTCCTTCTGC 	; Leng 09; Ind 0; Ind GGAAAAC	US-10-156-761-4577 L5 US-10-156-761-1 US-10-398-221-588 US-10-398-221-3598 US-10-156-761-3629 US-10-156-761-3629 US-10-156-761-5404 US-10-402-842-1 US-10-402-842-1 US-10-402-842-1 US-10-437-963-23116 US-10-437-963-201-1 US-10-437-963-50882 US-10-437-963-5997 US-10-437-963-991-1 US-10-437-963-991-1 US-10-437-963-991-1 US-10-437-963-991-7 US-10-437-963-991-7 US-10-437-963-991-1 US-10-437-963-991-1 US-10-437-963-991-1 US-10-437-963-991-1 US-10-437-963-991-1 US-10-437-963-991-1 US-10-437-963-991-1 US-10-437-963-991-1 US-10-437-963-991-1 US-10-671-434-106 US-10-671-49-106 US-10-671-49-106 US-10-671-134-106
CTTCTGCAGCCAGACCC 121 CTTCTGCAGCCAGACCC 121 CTTCCCCACCCTGAAGG 181	975; 0; Gaps CGCCCCTCCCCT 61	Sequence 4577, Ap Sequence 1588, Ap Sequence 3596, Ap Sequence 3596, Ap Sequence 342, Appl Sequence 34, Appl Sequence 34, Appl Sequence 14, Appl Sequence 1, Appli Sequence 1, Appli Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appli Sequence 17, Appli Sequence 18597, Ap Sequence 18597, Ap Sequence 18597, Ap Sequence 196339, Sequence 196339, Sequence 106339,

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Sequence 4691, Application US/10156761
PUBLICATION NO. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IXEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-10-156-761-4691
                                                            ANT: IKEDA, HARUO
ANT: ISHIKAWA, JUN
ANT: HORIKAWA, HIROSHI
ANT: SHIBA, TADAYOSHI
ANT: SAKAKI, YOSHIYUKI
ANT: SAKAKI, YOSHIYUKI
ANT: HATTORI, MASAHIRA
OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            962
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR TILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 4691
LENGTH: 939
TYPE: DNA
ORGANISM: Streptomyces avermitilis
PEATURE:
NAME/KEY: CDS
LOCATION: (1)..(939)
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                                                US/10156761
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Pred. No. 3.1e-16;
0; Mismatches 306;
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: ONURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
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; LOCATION: (4187715)
; OTHER INFORMATION: a, 1
US-10-156-761-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SHIBA, TĀDAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HAŢTORI, MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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ORGANISM: Streptomyces
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  CCCCTAGGGGCCTTCTGCCGGGGGAAGGAGGCCCCCGGGCGCGCTACCCCGCGCCCCAGGAAG
                                                                                                                               CGCAAGCTCGCCCGCGCTGCTCCCCGAGGACGAGAGCACCGCGTCCCGCTGGGCCGCC 5735952
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                                            GCGTCCATGGAGCTCGGCGCGCTGGTCTGCACGGCGAAGAACGAGACCTGCCACCGCTGC
                                                                                    GCCCTCATGGAGCTCGGGGCCACGGTCTGCCTGCCGAAACGGCCCCGTTGCGGGGCCTGC
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RESULT 4
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Publication No. US20040096863A1

GENERAL INFORMATION:
APPLICANT: Livuch, Zvi
APPLICANT: Paz-Elizur, Tamar
APPLICANT: Blumenstetin, Sara
TITLE OF INVENTION: METHODS AND KITS FOR DETERMINING A RISK TO DEVELOP CANCER, FOR E'
TITLE OF INVENTION: AN EFFECTIVENESS AND DOSAGE OF CANCER THERAPY AND FOR CORRELATIN
TITLE OF INVENTION: ACTIVITY OF A DNA REPAIR ENZYME AND A CANCER
FILE REFERENCE: 26315
FULL REFERENCE: 26315
CURRENT APPLICATION NUMBER: US/10/469,992
CURRENT FILING DATE: 2003-09-16
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
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Matches 299; Conservat
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                     GCCTCCTCCCGAGGGCGTGGACCCG------GGGGTGTGGAACCAGGCCCTCAT 518
                                                                                    GGAGCTCGGGGCCACGGTCTGCCTGCCGAAAACGGCCCGTTGCGGGGGCCTGCCCCTAGG 578
          GGCCTTCTGCCGGG 592
                                                  GGAGCTAGGGGCCACAGTGTGTACCCCACAGCGCCCACTGTGCAGCCAGTGCCCTGTGGA 1033
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Pred. No. 2.1e-14;
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 484
LENGTH: 1878
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US-09-925-301-484
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TITLE OF INVENTION: Nucleic Acids, Proteins and
FILE REFERENCE: PA106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: n equals a,t,g,
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NAME/KEY: misc feature
LOCATION: (1446)
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ORGANISM: Homo sapiens
      1049
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299; Conserv
   GAGCCTGTGCCGGG
                                                         eccerrereces 592
                                                                                                         GGAGCTAGGGGCCACAGTGTGTACCCCCACAGCGCCCACTGTGCAGCCAGTGCCCTGTGGA 1048
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                                                                                                                                                                                                                                                                                         GCCTCCTCCCGAGGGCGTGGACCCG------GGGGTGTGGAACCAGGCCCTCAT
                                                                                                                                                                                                                                                                                                                                                      GTGCCGTGTCCGAGCCATTGGTGCTGATCCCAGCAGCACCCTTGTTTCCCCAGCAGCTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCGGCTTTCCCTGGAAGAGGTCCTTAGGGTTCTTGCCAGGGGGCTACTACTACCGGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAGGCCCTCCCCTATTACCGCCGCTTTCTGGAGCGCTTTCCCCACCCTGAAGGCCCTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAGAAGGACCCTTACCGCGTCCTGGTCTCCGAGGTCCTTCTGCAGCAGACCCGGGTGGA 128
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Pred. No. 2.1e-14;
0; Mismatches 225;
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GENERAL INFORMATION:

APPLICANT: Berka, Randy M.

APPLICANT: Clausen, Ib Groth

TITLE OF INVENTION: Methods For Monitoring Multiple Gene

TITLE OF INVENTION: Expression

FILE REFERENCE: 10085.500-US

CURRENT APPLICATION NUMBER: US/09/974,300

CURRENT FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: 09/680,598

PRIOR APPLICATION NUMBER: 60/279,526

PRIOR APPLICATION NUMBER: 60/279,526

PRIOR FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 8481

SOFTWARE: FASTSEQ for Windows Version 4.0

1. SOFTWARE: FASTSEQ for Windows Version 4.0
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US-09-974-300-1583
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Best Local (
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Patent No. US2002
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LOCATION: (1)...(528)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Bacillus licheniformis
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 528
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Local Similarity 53.4%;
463
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                            TCGCC 426
                                                      CCTACAATCAGCCGGTCCCCCGCGGTAGACGGAAATGTCATGCGGGTCATGTCACGGATTC
                                                                         CCTTCGGGGAGCGGGTGGGCGGTGGACGGGAACGTCCGGAGGGTCCTCTCCCCGCCTCT
                                                                                                                                          TTTCC
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                                                                                                                                                                                                                                                       TCCCCTATTACCGCCGCTTTCTGGAGCGCTTTCCCACCCTGAAGGCCCTTGGCCGCGGCTT 196
                                                                                                                                                                                                                                                                                                                                                       ACCCTTATAAGGTGTGGGTGTCGGAAGTAATGCTTCAGCAGACGAGAGTGGACACGGTGA
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Pred. No. 8.5e-12;
0; Mismatches 183;
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RESULT 7

US-10-437-963-1325

Sequence 1325, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: LA ROSS, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua

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RESULT 8
US-10-425-114-32132
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APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221) B
CURRENT APPLICATION UNMERR: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 1325
SEQ ID NO 1325
LENGTH: 5850
                                                            GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION UNBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                      Sequence 32132, Application US/10425114 Publication No. US20040034888A1
                                               SEQ ID NO 32132
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Oryza sativa
                 TYPE: DNA
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ORGANISM: Zea mays
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nes 211; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                             563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCCCGTGGTCGACTACTACTCCCGGTGGATGGCCCGCTGGCCCACCGTGGACAGCC
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Pred. No. 1.2e-11;
0; Mismatches 168;
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; FEATURE:
; OTHER INFORMATION:
US-10-425-114-32132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
US-10-216-817-31
; ORGANISM: Mycobacterium tuberculosis US-10-216-817-31
                                                                              APPLICATION COMPOSITIONS AND METHODS FOR DETECTING MULTIDRUG TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING MULTIDRUG TITLE OF INVENTION: RESISTANT STRAINS OF M. TUBERCULOSIS HAVING MUTATIONS TITLE OF INVENTION: IN GENES OF THE mutT PAMILY FILE REPERENCE: 03495,0233-00000 CURRENT APPLICATION NUMBER: US/10/216,817 CURRENT FILING DATE: 2002-11-13 PRIOR APPLICATION NUMBER: 60/311,824 PRIOR APPLICATION NUMBER: 60/311,824 PRIOR APPLICATION NUMBER: 60/311,824 PRIOR PRIOR FILING DATE: 2001-08-14 PRIOR FILING DATE: 2001-08-14 PRIOR FILING DATE: 2001-08-14 PRIOR FILING DATE: 2001-08-21 NUMBER: FILING DATE: 2001-08-21 NUMBER: PATENTIN ONS: 32 SOFTWARE: PATENTIN VEY: 2.1
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Best Local Similarity
Matches 282; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31, Appropriate Publication No.
                                         LENGTH: 912
TYPE: DNA
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Pred. No. 4.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1660;
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Gaps

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APPLICATION NUMBER: 60/311,824
PRIOR PELICATION NUMBER: 60/311,824
PRIOR APPLICATION NUMBER: 60/313,523
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2001-08-21
SOPTWARE: PATENTIA NUMBER: 60/313,523
PRIOR FILING DATE: 2001-08-21
SOPTWARE: PATENTIA NUMBER: 60/313,523
PRIOR FILING DATE: 2001-08-21
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PRIOR FILING DATE: 2001-08-21
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PRIOR FILING DATE: 2001-08-21
LENGTH: 1312
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US-10-216-817-21
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Best Local S
Matches 345
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No. US20030129619A1
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Pred. No. 1.9e.
0; Mismatches
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                                                                                                                                                                                                                               Sequence 35788, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-10-437-963-35788
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APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 35788
LENGTH: 1425
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/10158844 Publication No. US20040029118A1 GENERAL INFORMATION:
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Best Local :
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                                      APPLICATION NUMBER: US/10/158,844
FILING DATE: 03-Jun-2002
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/961,527
FILING DATE: 1997-10-30
APPLICATION NUMBER: US 60/029,960
FILING DATE: 1996-10-31
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: Dell Latitude Pentium
OPERATING SYSTEM: Windows 98
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kunsch et al. TITLE OF INVENTION: Streptococcus NUMBER OF SEQUENCES: 391
                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   356
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STREET: 9410 Key West Ave
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCATAGCCTTCAATGAGGTTGTCCCTGTTGTGGACGGAAATGT 608
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55.7%;
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Pred. No. 2.1e-10;
                                                                                                                                                                                                                                                                                                                              Avenue
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                                                                                                                                              ; SEQ ID NO 46;
LENGTH: 968;
; TYPE: DNA
; ORGANISM: Micrococcus
US-09-864-866-46
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US-09-864-866-46
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                                                                                      Query Match
Best Local S
Matches 300
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 46, Application U
Patent No. US20020127656A1
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                                                                                                                                                                                                                        SOFTWARE: PatentIn version
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SEQUENCE CHARACTERISTICS:
LENGTH: 9909 base pairs
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hes 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID
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   104 TCCTTCTGCAGCAGACCCGGGTGGAGCAGGCCCTCCCCTATTACCGCCGCTTTCTGGAGC
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Similarity 47.2%;
                                ACCCGTACGCCGTCGCCGAGCTGGACTTCGAGACGCCGTTCGAGCTGCTCGTGGCCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09864866
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AACTTGCCTGAGCCAGCTGTAGATGGTAATGTCATGCGGGTCTTGGCGCGTCTGTTTG
                                                                                                          ATTTCCAGCTTGAAAGGGATTGGACCTTACACAGCAGCAGCCATTTCCAGTATTGCTTTT 5449
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                                                   GGGGAGCGGTGGCGGCGGTGGACGGGAACGTCCGGAGGGTCCTCTCCCCGCCTCTTCG 424
                                                                                                                                                                                                                       GCTGCAGCCCAGCAGATTATGACTGACTTTGGTGGCCAATTTCCAAATACCTATGAAGGA 5509
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                                                                                                                                                                CTTCGGGGGGCTTCCTGGGCCTTACACCGCGGCGGCGGTGGCCTCCATCGCCTTC 366
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APPLICANT: Lloyd, R. Stephen
APPLICANT: McCullough, Amanda K.
APPLICANT: McCullough, Amanda K.
APPLICANT: McCullough, Knoa
TITLE OF INVENTION: DNA REPAIR POLYPEPTIDES AN
FILE REFERENCE: 265.00170101
CURRENT APPLICATION NUMBER: US/09/864,866
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
NUMBER OF SEQ ID NOS: 49 ACGCCCGCCCCCCCCGCGGGGGGGAGAAGGACCCTTACCGCGTCCTGGTCTCCGAGG 103 Score 81.2; DB 9; Pred. No. 3e-09; 0; Mismatches 318 AND 318; METHODS Length Indels

18;

Gaps

163 259

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Sequence 1, Application US/10470565
; Publication No. US20040126870A1
; GENERAL INFORMATION:
APPLICANT: Societe des Produits Nestle S.A.
TITLE OF INVENTION: NCC2705 - the genome of a F
FILE REFERENCE: 80290/MO
; CURRENT APPLICATION NUMBER: US/10/470,565
; CURRENT FILING DATE: 2003-07-29
PRIOR APPLICATION NUMBER: EP 01102050.0
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2256646
; TYPE: DNA
; ORGANISM: Bifidobacterium longum
US-10-470-565-1
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US-10-470-565-1/c
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Best Local Similarity 52.5%;
Matches 218; Conservative
                                                                                             1487168 GGGCGTGCTGGTATCCGAAGTCATGAGCCAGCAGACGCAGATGAGCCGTGTAGTGCCGTA
                                                                                                                                                                                                                                                                             1487228 CGCATGGTGGGAGGCCAATGCGCGCGATTTGCCATGGCGCTTCGGCCGGGCCACGCCGTG 1487169
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TTACCGCCGCTTTCTGGAGCGCTTTCCCACCCTGAAGGCCCTGGCCGGCGGCTTCCCTGGA
                                                                                                                                                            CCGCGTCCTGGTCTCCGAGGTCCTTCTGCAGCAGACCCGGGTGGAGCAGGCCGCCCCTA 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 72.6; DB 17;
Pred. No. 6.2e-08;
0; Mismatches 179;
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APPLICANT: IKEDA, HARNOW
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.3%;
Best Local Similarity 47.1%;
Matches 305; Conservative
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSI
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Pred. No. 4.8e-07;
0; Mismatches 321;
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TIGHTOTEGGGCTTACACCGCGGGGGGTGGCTTCCATCGCTTCGGGGGAAGGGGTGGCTTCGGGGGGAAGGGGATGGCTTCGGGGGGGAAGGGGATGGCTTCGGGGGGAAGGCGATGGGGAAGGGGAAGGCCAAGGGGTGGACGGAAGGCCCAAGGGGTGGACGGAAGGCCCCAAGGGGTGGACCGAAGGCCCCAAGGCGTGGAAAGGCCCCAAGGCGGGGAAAGGCCCAAGGCGGGGGAAAGGCCCAAGGAAGGAAGAGAAGA	Db 744 CGGGGC Qy 621 GCCCAG	0y 561 CGGGGC	Db 627 TCCGGAA	Db 567 CACCGRO	381	507	Qy 321 TGGTCTC
	CGGGGCCTGCCCCATCGCCCGCTCTGCCCGGCGTACGGGGAGAGGGCGAGACCGACC	cTCGCACCATGTGATCTTCCACGGCCGCCGCATCTGTCACGCCCGCAAGCCGGCCTG CGGGGCCTGCCCCTAGGGGCCTTCTGCCGGGGAAGGAGGCCCCCGGGGGTACCCCGC	TCCGGACAAGATCGAGGCGCCCTCTGGGGGCGCGCTCTTCCCGAAGAGCGAGTGGACGATGCT GTGGAACCAGGCCCTCATGGAGCTCGGGGGCCACGGTCTGCCGAAAACGGCCCCGTTG	CAĆCĠĪĠĠĀĊACCCĀTTĪĊĆAĠCĠĠCTĊĠĪĊCĠĊĠĊTĠĢCAGTĠĢACCĠĀCGAĢAAGĀ GĀĢĀĀGĀĀĢĀŢĪTTCĢCCCTĢGCCAĞĞĞCTĊĢTCCTCCCGAĞĞĞĞCTĞACCĞĞĞĞĞT	GGCGGTGGACGGAACGTCCGGAAGGGTCCTCTCCCGCCTCTTCGCCCCGGGAAAGCCCCCAA	AGGACGCAAGACGGCCTTCGTGGTGCTCGGCAACG	rggrcrcgggccrracaccgcggcggcggcccrccarcgccrrcgggaagcgagraec

Search completed: October 8, 2004, 06:39:54 Job time : 591 secs



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Minimum
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Maximum Match 100%
Listing first 45 summaries
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/lab host="pH108 (phage-resistant)"
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/clone lib="NIH MGC 106"
/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1956)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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GGGTCTAGCCCAGCAGCTGGTGGACCCAGCCCGGCCAAGGAGGATTTCAACCAAGCAGAC
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                                                    GGGCCTCCTCCCCGAGGGCGTGGACCC------
                                                                                                                              TGTGCCGTGTCCGAGCCATTGGTGCTGATCCCAGCAGCACCTTGTTTCCCCAGCAGCTCTG
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nilarity 53.7%;
Conservative
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/clone_lib="NIH_MGC_48"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
/site_2: EcoRI; cDNA made by oilgo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GCCGAGCTTCGGGGGCTTCCTGGTCTCGGGCCTTACACCGCGGCGGCGGCGG
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4336498"
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Pred. No. 1.4e-05;
0; Mismatches 226
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MEDLINE
PUBMED
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Best Local Similarity 57.1%;
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1 (bases 1 to 496)
2 (
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300920 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
BG383035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 6 row: M column: 13
Seq primer: ATTTAGCTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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AGCGCTTCCCTGGAGGAGGTCAACCAGCTCTGGGCTGGCCTGGGCTATTACTCTCGAGGC 230
                                                            ACGGTGATCAACTACTACACCCGGTGGATGCAGACGTGGCCGACCCTGCGGGACCTGGCC
                                                                                                                                                                                    CAGGCCCTCCCCTATTACCGCCGCTTTCTGGAGCGCTTTCCCACCCTGAAGGCCCTGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab host="DH10B"
/clone_lib="MARC 1PIG"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2:
Library made from pooled tissue From day 11, 13, 1
and 30 embryos."
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|mol_type="mRNA"
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Pred. No. 1.8e-05;
0; Mismatches 143
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                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 922.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOAL004DA12QP1&cluster=922.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOAL004DA12QP1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 969)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX367285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Genoscope
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Homo sapiens cDNA clone
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CACTGTGATCAACTACTATACCGGATGGATGCAGAAGTGGCCTACACTGCAGGACCTGGC
                                         GCAGGCCCTCCCCTATTACCGCCGCTTTCTGGAGCGCTTTCCCACCCTGAAGGCCCTGGC 188
                                                                                                              GGAGAAGGACCCTTACCGCGTCCTGGTCTCCGAGGTCCTTCTGCAGCAGACCCCGGGTGGA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCCGCGTCCGAGCC 425
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                                                                                     GGACAGGCGGCATATGCTGTGTGGGTCTCAGAGGTCATGCTGCAGCAGACCCAGGTTGC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCCGCCTCTTCGCC 426
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                                                                                                                                                                                                                                                                                                                                                                         25-NORMALIZED"
                                                                                                                                                                                                                                                                                                                                                                                              /clone="CSODL004YB24"
/cell type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/cell line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
/mol_type="mRNA"
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                                                                                                                                                                                            10.2%;
                                                                                                                                                                     Score 99.4; DB 13;
Pred. No. 2.7e-05;
2; Mismatches 228;
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                                                                                                                                                                            Indels 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
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AGENCOURT_6627519 NIH_MGC_122
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1009)
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/clone_lib="NIH_MGC 122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: Not1; Site_2: EccNV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dr
primed and directionally cloned (EccNV site is destroyed
                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
/mol_type="mRNA"
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lone="IMAGE:5762392"
ab_host="DH10B"
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Best Local Similarity 53.3
Matches 289; Conservative
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Pred. No. 0.00012;
0; Mismatches 223;
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Contact: Robert Strausberg, | Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Co 맑 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. Consortium Gene Collection (MGC) (LLNL) EST 15-JUL-2002 ne IMAGE:6247891

sapiens

clone

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM2386 row: n column: 20 High quality sequence stop: 667.
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/tissue_type="ductal carcinoma, cell
/lab host="DH10B (phage_resistant)"
/clone_lib="NIH_MGC_110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 0.00039;
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Query Match
Best Local Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Verteb
Mammalia; Eutheria; Primates; Catarrhini; Homi
1 (bases 1 to 662)
NIH-MGC http://mgc.nci.nih.gov/.
National_natitutes of Health, Mammalian Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
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Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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GTGCCGTGTCCGAGCC
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                                                      CTCCCGCCTCTTCGCC 426
                                                                                                                                                                      GGCCTCCATCGCCTTCGGGGAGCGGGTGGCGGGGGGGGGAACGTCCGGAGGGTCCT
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                                                                                                                TGCCTCTATCGCCTTTGGNCAGGCAACCGGTGTGGTGGATGGCAACGTAGCACGGGTGCT
                                                                                                                                                                                                                                TACAGCAGAGCCCTGCAGCAGCTCCTGCCTGGCGTGGGGGCGCTACACAGCTGGGGCCAT
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//Clone lib="NIH MGC 115"
//Clone Torgan: pooled brain, lung, testis; Vector:
//notes="Organ: pooled brain, lung, testis; Vector:
//CMV-SPORTG; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon clonnig). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="DH10B"
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Pred. No. 0.00052;
D; Mismatches 150;
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIO157 row: n column: 15
High quality sequence stop: 577.
Location/Qualifiers
1 577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt,
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National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 577)
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602314663F1 NIH_MGC_85 Homo sapiens
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                                                       TGCCTCTATCGCCTTTGGCCAGGCAACCGGTGTGGTGGATGGCAACGTAGCACGGGTGCT
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ilarity 55.3%;
Conservative
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/lab_host="DH108 (phage-resistant)"
/clone_lib="NIH MGC_85"
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Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size_1.867 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
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Pred. No. 0.00062;
0; Mismatches 150;
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can )
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLAM11433 row: h column: 21
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TACAGCAGAGACCCTGCAGCAGCTCCTGCCTGGCGTGGGGGCGCTACACAGCTGGGGGCCAT
                                                                               CCGGCGGCTGCAGGAGGGAGCTCGGAAGGTGGTAGAGGAGCTAGGGGGCCCACATGCCACG
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                                    (bases 1 to 771)
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//clone lib="WIM MGC 115"
//clone lib="WIM MGC 115"
//note="Organ: pooled brain, lung, testis; Vector:
pCMV-SpORT6; Site 1: Not1; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1.3 kb, Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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/lab_host="DH10B"
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db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 1014)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bx401779 1014 bp mRNA linear EST 13-M Bx401779 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMA Homo sapiens cDNA clone CS0DL008YG02 5-PRIME, mRNA sequence. BX401779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODL008BD01QP1&cluster=922.r. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODL008BD01QP1.
Location/Qualifiers
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 922.r
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                     CACTGTGATCAACTACTATACCGGATGGATGCAGAAGTGGCCTACACTGCAGGACCTGGC
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CCGGCGGCTGCAGGAGGGAGCTCGGAAGGTGGTAGAGGAGCTAGGGGGCCACATGCCACG
                                          GGAACACCTCCACCGCCTGGCCCGAAGCGTGGAGGAGCTTCCCCCCGAGCTTC-----
                                                                                                                                                                                                                GCAGGCCCTCCCCTATTACCGCCGCTTTCTGGAGCGCTTTCCCCACCCTGAAGGCCCCTGGC 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="Homo sapiens B CELLS (RAMOS 25-NORMALIZED"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Nature 420, 563-573 (2002)

6 (bases 1 to 1933)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci, Adachi,J., Aizawa,K., Akimura,T., Hara,A., Hashizume,W., Furuno,M., Hanagaki,T., Hara,A., Hashizume,T., Hirozane,T., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoch,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,Nakamura,M., Nishi,K., Numazaki,R., Numazaki,R., Ohno,M., Ohsato,Nakamura,M., Nishi,R., Numazaki,R., Numazaki,R., Ohno,M., Ohsato,Nakamura,M., Nishi,R., Numazaki,R., Numazaki,R., Ohno,M., Ohsato,Nakamura,M., Nishi,R., Numazaki,R., Ohno,M., Ohsato,Nakamura,M., Numazaki,R., Ohno,M., Ohsato,Nakamura,M., Numazaki,R., Ohno,M., Ohsato,Nakamura,M., Ohsato,Nakamura,M., Numazaki,R., Ohno,M., Ohsato,Nakamura,M., Ohsato,
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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   CCTCCTCCCGAGGGCGTGG------ACCCGGGGGTGTGGAACCAGGCCCTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                GTGCCGTGTCCGGGCCATTGGTGCCGATCCCACCAGCACCCTTGTCTCTCATCACCTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

Direct Submission
                                                                                                                                                                                                                                                                      GGAACACCTCCACCGCCTGGCCCGAAGCGTGGAGGAGCTTCCCCCGAGCTTCG-----
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                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db xref="FANTOM DB:5730444C03"
/db_xref="MGI:2393728"
/db_xref="taxon:10090"
/clone="5730444C03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="whole body"
/clone_lib="RIKEN full-length enriched mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 90; DB 11;
Pred. No. 0.00078;
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BM921263
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Best Local :
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129 GCAGGCCCTCCCCTATTACCGCCGCTTTCTGGAGCGCTTTCCCACCCTGAAGGCCCTTGGC
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM12787 row: c column: 16
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1 (bases 1 to 1031)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
CAGTÉCTTCCCTGGAGGAGGTGAATCAACTCTGGGCTGGCCTGGGCTACTATTCTCGTGG
                                CACTGTGATCAACTATACCGGATGGATGCAGAAGTGGCCTACACTGCAGGACCTGGC
                                                                                                                                                                                                   GGACAGGCGGGCATATGCTGTGTGGGTCTCAGAGGTCATGCTGCAGGAGACCCAGGTTGC 380
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                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="NIM MGC 115"
/clone lib="NIM MGC 115"
/note="Organ: pooled brain, lung, testis; Vector:
pcMV-SpORT6; Site 1: Not1; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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Location/Qualifiers
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/clone="IMAGE:5752647"
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                                                                                                                                                                                                                                                                                                           Score 88.6; DB 12;
Pred. No. 0.0011;
0; Mismatches 219;
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BG761186.1 GI
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 900)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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602718527F1_NIH_MGC_49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
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                                 /tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage resistant)"
/clone_libe"NIH MCC 49"
/clone_libe"NIH MCC 49"
/clone_Torgan: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/corl; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI; cDNA sites using the following 5' adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II.RT [Life Technologies). Note: this is a NIH_MGC
                   Library.
                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                      lone="IMAGE: 4858374"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5-PRIME,
BX415111
                                                                                                                                                                                                                                                                                                                                                                                                              Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com http://fulllength.invitrogen.com/ InVitroGen Corporation 16(Faraday Avenue Genoscope sequence ID: CSOCAPOO4BE10QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 982)
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EST.
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/organism="Homo sapiens"

/mol_type="mtNA"

/mol_type="mtNA"

/db xref="teaxon:9606"

/clone="CSOCAP004YI20"

/tissue type="THYMUS"

/clone_Tib="Homo sapiens THYMUS"

/clone_Tib="Homo sapiens THYMUS"

/mote="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime and enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.

Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       982 )
o sapiens THYMUS h
a sequence.
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54.9%;
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Primates;
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Pred. No. 0.0
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.0016;
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e CSOCAPO04YI20
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Haloarcula marismortui
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                                                                                                  Email:
Seq pri
Class:
                                                                                                                                                                     Institute for Systems Biology
1441 North Street, Seattle,
Tel: 206 732 1412
Fax: 206 732 1299
                                                                                                                                                                                                                                                                                              Goo,Y., Roach,J., Glusman,G., Baliga,N.S., Deu DasSarma,S., Ng,W.V. and Hood,L. Low-pass Sequencing for Microbial Comparative Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                     Haloarcula marismortui
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Halobacteriaceae; Haloarcula.
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                                                                                                                      il: ygoo@systemsbiology.org
primer: M13 Forward
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                           GAAGGAGGCCCCCGGGCGCTACCCCGCGCC
                                                       CGCCTGCGAGAAAACGCCGGATTGTGACGGCGCACAGTGCCCCTGGCGCGAGTGGTGTTC
                                                                                                            GCTCATGCCAGCAGGCAGTCGCGGGTCTGGAACAACGCTATCATGGAATTGGGTGGTGT
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/db xref="taxon:2238"
/clone lib="Hm pUC18 Library"
/note="Vector: pUC18; Site 1: SmaI; A shotgun
constructed from Haloarcular marismortui genom
pUC18/SmaI/BAP plasmid"
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Search completed: March 4, 2004, 05:46:54 Job time: 2403 secs

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Result
No.
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Maximum DB seq
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Maximum Match 100%
Listing first 45 summaries
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         US-09-938-901-1
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length: 2000000000
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| (gn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
| (gn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| (gn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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14 US-10-156-761-4691
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                                                                                                                US-09-925-301-484

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Sequence 1, Appli
Sequence 4691, Ap
Sequence 1, Appli
Sequence 3183, Ap
Sequence 32132, A
Sequence 31, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 46, Appl
Sequence 4577, Ap
Sequence 1588, Appl
Sequence 1588, Appl
Sequence 1588, Appli
Sequence 1588, Appli
Sequence 3596, Ap
Sequence 3596, Ap
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US-10-205-032-15	c	US-10-156-761-3783	US-09-938-901-7	US-10-671-419-1	US-10-671-403-1	US-10-671-419-3	US-10-671-403-3	US-10-156-761-2469	US-10-156-761-4189	US-10-156-761-6400	US-10-671-419-106	US-10-671-403-106	US-10-156-761-4667	US-09-864-408A-9041	US-10-205-032-1	US-10-205-032-19	US-09-938-901-5	US-10-424-599-105239	US-09-938-901-1	US-10-289-762-1	ď		US-09-070-927A-17	US-10-402-842-1	US-10-402-842-3	US-10-156-761-5404	US-10-329-079-34	US-10-329-079-42
Sequence 15, Appl	Sequence 7, Appli	Sequence 3783, Ap	Sequence 7, Appli	Sequence 1, Appli	Sequence 1, Appli	u ,	Sequence 3, Appli	246	4189,	Sequence 6400, Ap	106,	106,	Sequence 4667, Ap	9041,		19	ა	105	,	Sequence 1, Appli	1, 1	23,	17,	۳	Sequence 3, Appli	54	Sequence 34, Appl	Sequence 42, Appl

ALIGNMENTS

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NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 975
TYPE: DNA
ORGANISM: Thermus thermophilus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(975)
US-09-938-901-1
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Best Local Similarity 100.0%; Pred. No. 5e-199;
Matches 975; Conservative 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09938901 Publication No. US20030008291A1
                                                                                                                                                                                                                                                                                                          121 CGGGTGGAGCAGGCCCTCCCCCTATTACCGCCGCTTTCTGGAGCGCTTTCCCCACCCTGAAG
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                                                            61 TGGCGGGGGAGAAGGACCCTTACCGCGTCCTGGTCTCCGAGGTCCTTCTGCAGCAGACC 120
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                                        120
                180
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RESULT 2
US-10-156-761-4691
Sequence 4691, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: ISHIKAWA, HARUO
APPLICANT: HORIKAWA, HUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HORIKAWA, HORIKUKI
APPLICANT: HORIKAWA, HORIKUKI
APPLICANT: HORIKAWA, HORIKUKI
APPLICANT: HORIKAWA, HORIKUKI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
ITITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 4691
LENGTH: 939
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAMEKEY: CDS
LOCATION: (1)..(939)
US-10-156-761-4691
RESULT 3
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
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GENERAL INFORMATION:

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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UF 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: UF 2001-272697
PRIOR PILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
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OTHER INFORMATION: a, t,
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US-09-925-301-484
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APPLICANT: Rosen et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 484, Application US/09925301 Patent No. US20020052308A1
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA106
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LOCATION: (1446)
OTHER INFORMATION: n equals a,t,g,
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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 GGAGCTAGGGGCCACAGTGTGTACCCCACAGCGCCCACTGTGCAGCCAGTGCCCTGTGGA 104
                                                                                                                                          GTGCCGTGTCCGAGCCATTGGTGCTGATCCCAGCAGCACCCTTGTTTCCCAGCAGCTCTG
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Pred. No. 1.6e-13;
0; Mismatches 225;
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GCCTTCTGCCGGG

592

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APPLICANT: Berks, Randy M.

APPLICANT: Clausen, Ib Groth
ITILE OF INVENTION: Methods For Monitoring Multiple Gene
ITILE OF INVENTION: Expression
ITILE OF INVENTION: Expression
ITILE OF INVENTION: Expression
ITILE OF INVENTION INVESTION
ICURRENT APPLICATION NUMBER: US/09/974,300
ICURRENT FILING DATE: 2001-10-05
IPRIOR APPLICATION NUMBER: 09/680,598
IPRIOR APPLICATION NUMBER: 60/279,526
IPRIOR APPLICATION NUMBER: 60/279,526
IPRIOR APPLICATION NUMBER: 60/279,526
IPRIOR APPLICATION NUMBER: 50/279,526
IPRIOR FILING DATE: 2001-03-27
INUMBER OF SEQ ID NOS: 8481
ISOSTMARE: FastSEQ for Windows Version 4.0
ISEQ ID NO 1583
INDER ON DATE: 208
RESULT 6
US-10-425-114-32132
; Sequence 32132, A
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; NAME/KEY: misc feature
; LOCATION: (1)...(528)
; OTHER INFORMATION: n =
US-09-974-300-1583
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US-09-974-300-1583
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Best Local Similarity
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Pred. No. 5.1e-11;
0; Mismatches 183;
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Application US/10425114

RESULT 7
US-10-216-817-31
; Sequence 31, Application US/10216817
; Publication No. US20030129619A1
; GENERAL INFORMATION:

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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)8
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT SILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 32132
LENGTH: 1660
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Best Local Similarity
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ORGANISM: Zea mays
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 GGCCTTCTGCCGGGG
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ilarity 50.7%;
Conservative
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Pred. No. 2.4e-10;
0; Mismatches 253;
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RESULT 8
US-10-216-817-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING MULTIDRUG TITLE OF INVENTION: RESISTANT STRAINS OF M. TUBERCULOSIS HAVING MUTATIONS FILTED FINDERS OF THE MULT FAMILY FILE REFERENCE: 03495.0233-00000 CUBRENT APPLICATION NUMBER: US/10/216,817 CURRENT FILING DATE: 2002-11-13 PRIOR APPLICATION NUMBER: 60/311,824 PRIOR APPLICATION NUMBER: 60/311,824 PRIOR APPLICATION NUMBER: 60/313,523 PRIOR APPLICATION NUMBER: 60/313,523 PRIOR FILING DATE: 2001-08-14 PRIOR PRIOR DATE: 2001-08-12 PRIOR FILING DATE: 2001-08-21 NUMBER: FALENTIN VET. 2.11 SEQ ID NO 31 LENGTH: 912
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Matches
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nes 345; Conserv
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                                                                                                                         CGGCATGCCGGTTATCCGCCGTCGGACGGTCC--
                                                                                                                                                     GGGAAGGACCCCCCGGGCGCTACCCCGCGCCAGGAAGCGCCGGGGGAAGGAGGAGCGC
                                                                                                                                                                                                                   ACGGTCTGCCTGCCGAAACGGCCCCGTTGCGGGGCCTGCCCCTAGGGGGCCTTCTGCCGG
                                                                                                                                                                                                                                                   CTGTTGCCGCACCGCGAGACGGCGCCTGAATTTTCGGTCGCGCTGATGGAGTTGGGTGCG
                                                                                                                                                                                                                                                                                CTCCTCCCGAGGGCGTGGACCCGGGGGGTGTGGAACCAGGCCCTCATGGAGCTCGGGGCC
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                                                                                          CTCGTCGCCCTCGTCCTCGGGCGG 678
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                                                                                                                                                                                     ACGGTGTGCACCGCCCGCACACCCCGGTGCGGGTTATGCCCGCTGGACTGGTGCGCATGG
                                                                                                                                                                                                                                                                                                                                                                             TACCGCCAGCGGGTGCCGGTGGTGGACACCAATGTGCGGCGCGTGGTGGCCCGCGCCGTT
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nilarity 50.2%;
Conservative
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Pred. No. 9.6e-10;
0; Mismatches 309;
                                                                                                                           -GCCGCGCGGGGGGCAGGCCTACACC
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; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-216-817-21
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Publication No. US20030129619A1

GENERAL INFORMATION:

APPLICANT: GICQUEL, BRIGITTE

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING MULTIDRUG

TITLE OF INVENTION: RESISTANT STRAINS OF M. TUBERCULOSIS HAVING MUTATIONS

TITLE OF INVENTION: IN GENES OF THE mutT FAMILY

FILE REFERENCE: 03495,0233-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. SEQ ID NO 21
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Best Local Similarity
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CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 60/311,824
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: 60/313,523
PRIOR APPLICATION NUMBER: 60/313,523
PRIOR FILING DATE: 2001-08-21
NUMBER OF SEQ ID NOS: 32
 918
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   GGAACCGACCGCCAAGTCCGCGGACGG
                                                                                 GGGAAGGAGCCCCCGGGCGTACCCCCGCGCCCAGGAAGGCGCCGGGCGAAGGAGGAGCGC
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                                                             CGGCATGCCGGTTATCCGCCGTCGGACGGTCC
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                                                                                                                                                     ACGGTCTGCCTGCCGAAAACGGCCCCGTTGCGGGGCCTTGCCCCTAGGGGGCCTTCTGCCGG
                                                                                                                                                                                     CTGTTGCCGCACCGCGAGACGGCGCCTGAATTTTCGGTCGCGCTGATGGAGTTGGGTGCG
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nilarity 50.2%;
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                                                                GCCGCGCGGGGGCAGGCCTACACC
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Best Local (
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Publication No. US20040029118A1
GENERAL IMPORMATION:
APPLICANT: Kunsch et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PB340P1D1
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/158,844

FILING DATE: 03-Jun-2002

CLASSIFICATION: UNKnown>

PRIOR APPLICATION UNMBER: US 08/961,527

APPLICATION NUMBER: US 60/029,960

FILING DATE: 1997-10-30

APPLICATION NUMBER: US 60/029,960

FILING DATE: 1996-10-31

ATTORNEY/AGENT INFORMATION:

NAME: Human Mart.
                                                                                                                                                                                                                                                                                                                                                                      , Match
B.4%; Score 82; DB 12; Length 9909;
Local Similarity 52.2%; Pred. No. 5.7e-09;
les 218; Conservative 0; Mismatches 185; Indels 1
                                                                                                 5568
                                                                                                                                          5628 GAGAGTTTACTGAAAGCTTGGGAGGGCTTGGGCTATTATTCTCGAGTTCGCAATATGCAG
                                                                                                                                                                                                5688 TACTACGAAAGATTTTTGGACTGGTTTCCAACTGTCGAAAGTCTGGGAACTGCGCCTGAG
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                                                                     307
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                                                                                                                                                                                    202
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MEDIUM TYPE: CD-R
COMPUTER: Dell Latitude Pentium
OPERATING SYSTEM: Windows 98
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:

ADDRESSES: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                82
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GGGGAGCGGGTGGCGGTGGACGGGAACGTCCGGAGGGTCCTCTCCCGGCCTCTTCG 424
                           ATTTCCAGCTTGAAAGGGATTGGACCTTACACAGCAGGAGCCATTTCCAGTATTGCTTTT 5449
                                                                                                              GCGGAAACACCTCCACCGCCTGGCCCGAAGCGTGGAGGAGCTTCCCCCGAGCTTCGCCGAG
                                               GCTGCÁGCCCAGCAGATTATGACTGACTTTGGTGGCCAATTTCCAAATACCTATGAAGGA 5509
                                                                                                                                                                           GAAGAGGTCCTTAGGGTCTGGCAGGGGGGGGGCTA---
                                                                                                                                                                                                                       TATTACCGCCGCTTTCTGGAGCGCTTTCCCACCCTGAAGGCCCTGGCCGCGGCTTCCCTG 201
                                                                                                                                                                                                                                                                           TACCGCGTCCTGGTCTCCGAGGTCCTTCTGCAGCAGACCCGGGTGGAGCAGGCCCTCCCC 141
                                                                                                                                                                                                                                                                                                              CTTCTCGCTTGGTATGATGAAAACAAAAGAGATTTGCCTTGGAGGAGAAGTAAAAATCCT
                                                                                                                                                                                                                                                       TATČAČAŤĊTGĠĠŤAŤĊTĠAAAŤĊAŤGĊŤTĊĀĠĊĀĠĀĊĊĀĠĠĠŤĠĠĀTACĀĠTTAŤĊĊĊT 5689
                                                                                                                                                                                                                                                                                                                                         LENGTH: 9909 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hyman, Mark J. REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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US-09-864-866-46
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Sequence 46, Application US/09864866
Patent No. US20020127656A1
GENERAL INFORMATION:
APPLICANT: Lloyd, R. Stephen
APPLICANT: McCullough, Amanda K.
APPLICANT: MCCUllough, Amanda K.
APPLICANT: Nguyen, Khoa
FITLE OF INVENTION: DNA REPAIR POLYPEPTIDES ANI
FILE REFERENCE: 265.00170101
CURRENT APPLICATION NUMBER: US/09/864,866
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/206,279
PRIOR APPLICATION NUMBER: US 60/206,279
PRIOR FILING DATE: 2000-05-23
NUMBER OF SEQ ID NOS: 49
SEQ ID NOS 46
ILNOTHER: PatentIn Version 3.0
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; TYPE: DNA
; ORGANISM: Micrococcus
US-09-864-866-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.3%;
Best Local Similarity 47.2%;
Matches 300; Conservative
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                                                                                                                                                                                                                                                         266 TGGCCCGAAGCGTGGAGGAGCTTCCCCCGAGCTTCCGCGAGCTTCCGGGGGCTTCCTCGTC 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5448 AACTTGCCTGAGCCAGCTGTAGATGGTAATGTCATGCGGGGTCTTGGCGCGCGTCTGTTTG 5391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 ACGCCCGCCCCCCCCCCGCGGGGGGGAGAAGGACCCCTACCGGGTCCTGGTCTCCGAGG 103
CGCGCGCCCTGCTGGCCTACGAGCTCAAGCCCGGCC 835
                                          GGAAGCGCCGGGCGAAGGAGGAGCGCCTCGTCGCCC 661
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                                                                               GGTGCCCGATCGCCCGCTGGTGCCCGTCCTACGCCGGGGGGAGACCGAACCGAACCGG
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Pred. No. 1.3e-08;
0; Mismatches 318;
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US-10-156-761-4577

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; NAME/KEY: CDS
; LOCATION: (1)..(930)
US-10-156-761-4577
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APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
FULE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
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SEQ ID NO 4577
LENGTH: 930
TYPE: DNA
ORGANISM: Streptomyces ave:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4577, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
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APPLICANT:
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CGGGGCCTGCCCCTAGGGGCCTTCTGCCGGGGGAAGGAGGCCCCCGGGCGCTACCCCGC 620
                                                                                                                                                                                                                                                                                                   GGAGAAGGAGCTTTTCGCCCTCGCCCAGGGCCTCCTCCCCGAGGGCCTGGACCCCGGGGGT
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HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHEA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, WASHAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH
APPLICANT: SHIBA, TADAYOSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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LOCATION: (4187715)
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TYPE: DNA
ORGANISM: Streptomyces
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hes 305; Conserv
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441 GGAGAAGGAGCTTTTCGCCCCTCGCCCAGGGCCTCCCCCCGAGGGCGTGGACCCCGGGGGT 500
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                                                                   CACCGTGGACACCCATTTCCAGCGGCTCGTCCGCCGCTGGCAGTGGACCGACGAGAAGGA 5607842
                                                                                                           GGCGGTGGACGGGAACGTCCGGAGGGTCCTCTCCCGCCTCTTCGCCCGGGAAAGCCCCCAA 440
                                                                                                                                                    CGGCGTAGGACGCCAAGACGGCCTTCGTGGTGCTCGGCAACGCCTTCGGGCGGCCCCGGCAT 5607782
                                                                                                                                                                                 TGGTCTCGGGCCTTACACCGCGGCGGCGGTGGCCTCCATCGCCTTCGGGGAGCGGGTGGC 380
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                                                                                                                                                                                                                                                                                                                            CCTCCGGCCCACCGGCTTCTTCCGGGCCAAGACCAAGTCGGTCATAGGGCTGTCCAAGGC 5607662
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Pred. No. 2.6e-07;
0; Mismatches 321;
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US-10-398-221-1588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVESTION: Listeria innocua, genome and
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398, 221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
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US-10-398-221-1588
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Best Local Similarity
Matches 215; Conserv
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SEQ ID NO 1588
LENGTH: 991
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Publication No. US20040018514A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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               GCCCGCGTTTTAG
                                            TCCCGCCTCTTCG 424
                                                                  TTGAGTATTĞÜÜTA ÇAACCAAGCTĞAACCAĞ ÇAĞTĞĞATĞĞ ÇAATĞTTATĞ ÇĞTĞTÇATÇ
                                                                                         GCCTCCATCGCCTTCGGGGAGCGGGTGGACGGGGAACGTCCGGAGGGTCCTC 411
                                                                                                                             ACCGACTTAACCACTATTTTATCGCTTAAAGGTGTGGGACCGTATACAGCCGGAGCTATC
                                                                                                                                                                                       GTCAGAAACCTCCAAACAGCCATGAAGCAAGTGATGGCCGATTTTTCTGGAGAAGTTCCT
                                                                                                                                                                                                                   GCGGAACACCTC------CACCGCCTGGCCCGAAGCGTGGAGGAGCTTCCC 291
                                                                                                                                                                                                                                                 GTCCAAGCGGATGAAGCGGATATTTTAAAAGCGTGGGAAGGCTTAGGCTATTATTCTCGT
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ilarity 49.7%;
Conservative
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Pred. No. 7.9e-06;
0; Mismatches 203;
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US-10-156-761-3629
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Sequence 3629, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: ONURA, SATOSHI
APPLICANT: IKEDA, HARUO
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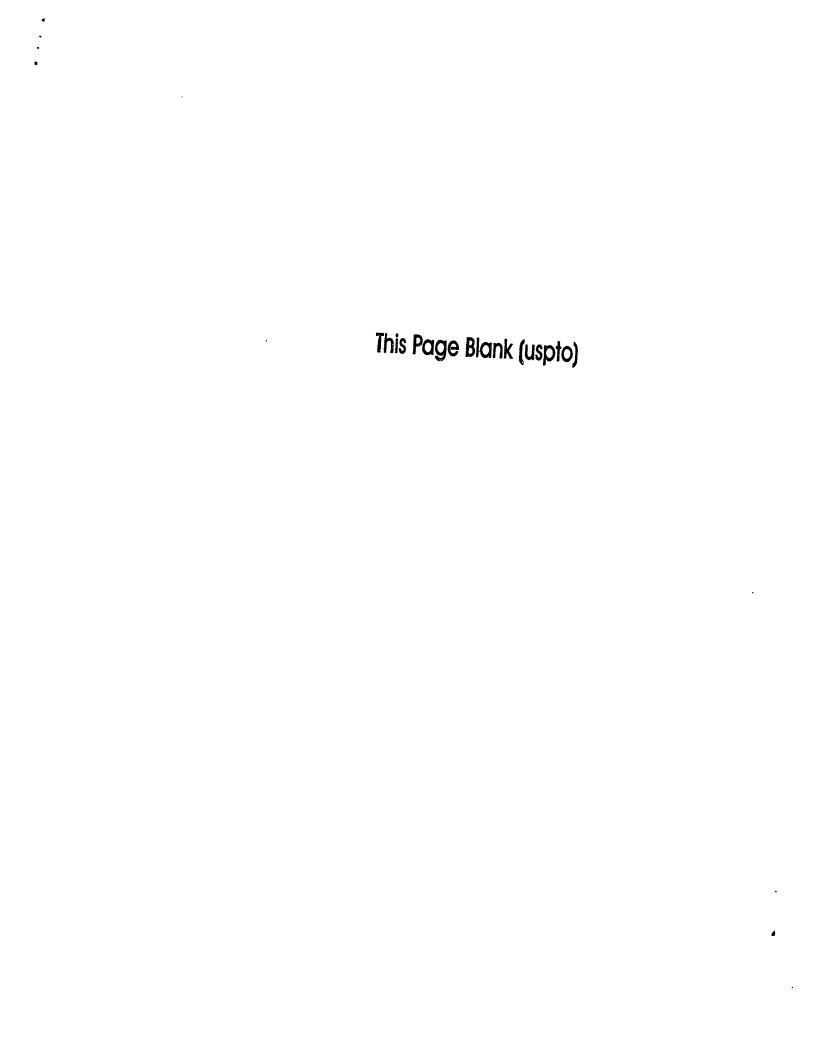
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Sequence 3596, Application US/10398221

| Sequence 3596, Application US/10398221
| Publication No. US20040018514A1
| GENERAL INFORMATION:
| APPLICANT: KINST, Frederik
| APPLICANT: GLASER, Philippe
| TITLE OF INVENTION: Listeria innocua, genome and
| FILE REFERENCE: 344 702 - US
| CURRENT APPLICATION NUMBER: US/10/398,221
| CURRENT FILING DATE: 2003-03-27
| PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
| PRIOR FILING DATE: 2001-10-04
| PRIOR FILI
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; TYPE: DNA
; PEATURE:
; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(end)
; OTHER INFORMATION: n can be any nucleotide: a,g,c
US-10-398-221-3596
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Best Local
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                                                                 412 TCCCGCCTCTTCG
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Similarity 49.7%;
15; Conservative
GCCCGCGTTTTAG 1145
                                                                                                                       TTGAGTATTGCCTACAACCAAGCTGAACCAGCAGTGGATGGCAATGTTATGCGTGTCATC
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Pred. No. 6.2e-06
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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OP INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-97
PRIOR FILING DATE: 2001-09-97
PRIOR FILING DATE: 2001-08-97
PRIOR FILING DATE: 2001-09-97
PRIOR FILING DA
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TYPE: DNA
CORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(11058)
US-10-156-761-3629
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Best Local Similarity 48.9%;
Matches 278; Conservative
7159
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CTGAGCGTGCTGACCGAGGAGGACCGCT
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Search completed: March Job time : 1286 secs

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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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US-09-252-991A-6783
US-09-489-039A-4788
US-09-489-039A-6783
US-09-651-656-38
US-09-651-656-38
US-09-651-656-38
US-09-103-840A-2
3 US-09-103-840A-2
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; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6886
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TILLE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6886
LENGTH: 1401
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Best Local Similarity
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Patent No. 6551795
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Pred. No. 2.2e-16;
0; Mismatches 231;
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APPLICANT: MARC J. Rubenfield and AMINO ACID SEQUENCES RELATING TO E

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO E

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 6739

LENGTH: 1413

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa
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; ORGANISM: Klebsiella
US-09-489-039A-4788
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US-09-489-039A-4788
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GENERAL INFORMATION:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6551795
                                                         STATE:
                                          COUNTRY:
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Best Local Similarity
Matches 248; Conserv
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 CTGAAGGCCCTGGCCGCGCTTCCCTGGAAGAGGTCCTTAGGGTCTGGCAGGGGGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 CAGACCCGGGTGGAGCAGGCCCTCCCCTATTACCGCCGCTTTCTGGAGCGCTTTCCCACC
                                                                                                         AAGCGCGTACTGGCGCTACCTGGCGCAGGACGGCTATCCCGGCGAACCGAAGGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCGAGGCACTGGCCGGCGGCCGAGGACGAAGTCCTGCACCTGTGGACCGGGCTCGGC
AGGGCGCTGTGGGAAGCCCGCCGAACGCTTCACCCCG
                                                CTCGCCCAGGGCCTCCTCCCCGAGGGCGTGGACCCG 495
                                                                                                                                                             CGGAGGGTCCTCTCCCGCCTCTTCGCCCGGGAAAGCCCCCAAGGAGAAGGAGCTTTTCGCC
                                                                                                                                                                                                                                                                                                                                                                                    GAGGAGCTTCCCCCGAGCTTCGCCGAGCTTCGGGGGCTTCCTGGTCTCGGGCCTTACACC
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                                                                                                                                                                                                                      GCTGGAGCCATCGCCAGCCTGTCGATGGGCCTGCGCGCACCGATCCTCGACGGCAACGTC
                                                                                                                                                                                                                                                                                                                                GGGGAGTTCCCCCGCGACGTCGAGCAACTCGCCGAACTGCCCGGCATCGGCCGCTCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACTACCGGCGGGCGGAACACCTCCACCGCCTGGCCCGAAGCGT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGCCCTGGCAGCAGGGCATCACCCCCTACCGGGTGTGGGTCTCGGAAATCATGCTGCAG
                                                                                                                                                                                                                                                                          GCGGCGGCGGTGGCCTCCATCGCCTTCGGGGAGCGGGTGGCGGCGGTGGACGGGAACGTC
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Pred. No. 7.6e-13;
0; Mismatches 193;
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S-08-813-574-1
Sequence 1, Application US/08813574
Patent No. 6013473
Patent No. 6013473
GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fei
TITLE OF INVENTION: Human MutY
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

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Query Match
Best Local S
Matches 299
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/013,132
PILING DATE: 11-MAR-1996
ATTORNEY, AGENT INFORMATION:
NAME: Han, William T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1858 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: cDNA
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REFERENCE/DOCKET NUMBER: ATT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Local Similarity 54.0%;
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1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            498 GGACAGGCGGGCATATGCTGTGTGGGTCTCAGAGGTCATGCTGCAGCAGACCCAGGTTGC
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GAGCCTGTGCCGGG 1051
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                                              GGCCTTCTGCCGGG
                                                                                                                                           GGAGCTCGGGGCCACGGTCTGCCCTGCCGAAAACGGCCCGTTGCGGGGGCCTGCCCCTAGG
                                                                                                                                                                                             GGGTCTAGCCCAGCAGCTGGTGGACCCAGCCCGGCCAGGAGATTTCAACCAAGCAGCCAT
                                                                                                                                                                                                                                                                                               GTGCCGTGTCCGAGCCATTGGTGCTGATCCCAGCAGCACCCTTGTTTCCCCAGCAGCTCTG
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                                                                                             GGAGCTAGGGGCCACAGTGTGTACCCCACAGCGCCCACTGTGCAGCCAGTGCCCTGTGGA 1037
                                                                                                                                                                                                                                              GGCCTCCTCCCGAGGGCGTGGACCCG-------GGGGTGTGGAACCAGGCCCTCAT
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US-09-650-855-38
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; ORGANISM: Escherichia coli
US-09-651-656-38
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SEQ ID NO 38
LENGTH: 2293
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Patent NO. 6340566
GRMERAL INFORMATION:
APPLICANT: MCCUTHEN-MALONEY, SANDRA
APPLICANT: LAWRENCE LIVERNORE NATIONAL LABORATORY
APPLICANT: LAWRENCE LIVERNORE NATIONAL LABORATORY
TITLE OF INVENTION: DETECTION AND QUANTITATION OF SINGLE NUCLEOTIDE
TITLE OF INVENTION: POLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTATIONS,
TITLE DEFENSACE. TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
                                                                                                                                                                                                                                                                                             Sequence 38, Application US/09650855 Patent No. 6365355 GENERAL INFORMATION:
SOFTWARE:
SEQ ID NO 38
                                   APPLICANT: MCCUTHEN-MALONEY, SANDRA
APPLICANT: LAWRENCE LIVERNOR NATIONAL LABORATORY
APPLICANT: LAWRENCE LIVERNOR NATIONAL LABORATORY
ITTLE OF INVENTION: CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA
ITTLE OF INVENTION: MUTATIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND DNA
ITTLE OF INVENTION: MISMATCHES
FILE REFERENCE: IL-10284
CURRENT APPLICATION NUMBER: US/09/650,855
CURRENT FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: 60/192,764
PRIOR FILING DATE: 2000-03-28
NUMBER: OF SEQ ID NOS: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.9%;
Best Local Similarity 54.1%;
Matches 210; Conservative
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CURRENT APPLICATION NUMBER: US/09/651,656
CURRENT FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: 60/192,764
PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 106
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Pred. No. 7.2e-09;
0; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425
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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-24007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 2
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US-09-103-840A-2
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Best Local Simi
Matches 210;
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                                                                                                                                                   Query Match
                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
-09-103-840A-2
                                                                                                                                                                                                                                                                                                         LENGTH: 4403765
TYPE: DNA
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TYPE: DNA
ORGANISM: Escherichia
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                                         4022631
                                                                                                              / Match 8.9%;
Local Similarity 50.2%;
hes 345; Conservative
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                                     CTTCTCGCTTGGTATCAGCGATCGCACCGGGATCTGCCCTGGCGAGAGCCCCGGTGTCAGC 4022690
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   CCTTACCGCGTCCTGGTCTCCGAGGTCCTTCTGCAGCAGACCCGGGTGGAGCAGGCCCTC 138
                                                                          TCANACGCGTGCTGGCGCGCGCTATGC 1548
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ilarity 54.1%;
Conservative
                                                                                                              Score 86.6; DB 3;
Pred. No. 1.8e-08;
0; Mismatches 309;
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Pred. No. 7.2e-09;
0; Mismatches 163; Indels
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CTCCTCGCCTGGTACCGGGAAAAACGCCCGCCCCCTCCCCTGGCGGGGG---GAGAAGGAC 78

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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/99/103,840A
CURRENT APPLICATION NUMBER: US/99/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIN Ver. 2.1
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US-09-103-840A-1
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GENERAL INFORMATION:
                      Query Match
Best Local
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                                                                                  -09-103-840A-1
                                                                                                 ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
                                                                                                                                          TYPE: DNA
                                                                                                                                                          LENGTH: 4411529
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  8.9%;
llarity 50.2%;
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    <u>..</u>
Score 86.6; DB 3;
Pred. No. 1.8e-08;
0; Mismatches 309;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
                  APPLICATION NUMBER: U
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                               ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
COMPUTER: MSDOS Version 6.2
                                                                                                                                        COMPUTER: HP Vectra 48
OPERATING SYSTEM: MSDO:
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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CITY: Rockville
STATE: Maryland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGTTGCCGCACCGCGAGACGGCGCCTGAATTTTCGGTCGCGCTGATGGAGTTGGGTGCG
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US-09-107-532A-3654
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TOPOLOGY:
US-08-961-527-12
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3654, Application US/09107532A
Patent No. 6580275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.4%;
Best Local Similarity 52.2%;
Matches 218; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 9909 base pairs
TYPE: nucleic acid
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REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
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OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5448
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ADDRESSEE: GENOME THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                        CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                              COMPUTER:
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                                                                                                                                                                                                      ZIP: 02354
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and David Bush AND AMINO ACID SEQUENCES RELATING FAECIUM FOR DIAGNOSTICS AND THERAN

AND THERAPEUTICS

CORPORATION

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AACTTGCCTGAGCCAGCTGTAGATGGTAATGTCATGCGGGTCTTGGCGCGTCTGTTTG 5391
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                                                                                                        ATTTCCAGCTTGAAAGGGATTGGACCTTACACAGCAGGAGCCATTTCCAGTATTGCTTTT 5449
                                                                                                                                                         GCTGCAGCCCAGCAGATTATGACTGACTTTGGTGGCCAATTTCCAAATACCTATGAAGGA 5509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATCACATCTGGGTATCTGAAATCATGCTTCAGCAGACCAGGGTGGATACAGTTATCCCCT 5689
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Pred. No. 8.6e-08;
0; Mismatches 185
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PRIOR APPLICATION DATA:

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TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3654
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
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Similarity 47.6%;
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                                                                      CCGAMACGGCCCCGTTGCGGGGCCTGCCCCCTAGGGGCCTTCTG
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                                                                                                                                            GAAAAGCATCCAGGTGAATTCAACCAAGCAATGATGGATCTAGGTTCAGCTATCTGTACA 63
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   CCAACTTCTCCAAAGTGTGAGACTTGTCCGATCCAAGCCTTTTG
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Pred. No. 0.00029;
0; Mismatches 279
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APPLICANT: Susan E. Jensen
APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence En
TITLE OF INVENTION: Acid Biosynthes
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:

Encoding

Enzymes

of Clavulanic

ADDRESSEE:

JACOBSON, PRICE, HOLMAN & STERN, PPLC

Acid Biosynthesis 25

Sequence 23, Application US/09385028 Patent No. 6232106 GENERAL INFORMATION:

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US-09-134-000C-1710
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US-09-134-000C-1710
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Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 03796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US/0955,778

PRIOR FILING DATE: 1997-08-15

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812
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                                                                   GCCGTTTATTTG
                                                                                                   CCCGCCTCTTCG
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ilarity 48.8%;
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Pred. No. 0.0005;
0; Mismatches 206;
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SEQUENCE CHARACTERISTICS:
LENGTH: 127 base pairs
LENGTH: 127 base pairs
LENGTH: 127 base pairs
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic
US-09-385-028-23
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APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. Douglas Price
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P5745
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Pred. No. 0.00055;
0; Mismatches 423;
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LENGTH: 1227 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-726-614-23
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US-09-726-614-23
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APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6514735
PITLE OF INVENTION: Acid Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23, Application Patent No. 6514735
                                                                       Matches
                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPUTER: DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,614
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APPLICANT: Susan
                                                                                                                                                                                                                                                 TELEX: RCA 248593 IDEA UR INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. Douglas Price
REGISTRATION NUMBER: 24,51
                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-6666
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ZIP: 20004
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CITY: Washington
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TELEFAX: (202) 39305350
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                                                                     Conservative
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                                                                                                                                                            DNA (genomic)
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                                                                       Score 62.2; DB 4;
Pred. No. 0.00055;
0; Mismatches 423;
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GTCTGGCAGGGGGCGGCTACTACCGGCGGGCGGAACACCTCCACCGCCTGGCCCGAAGC 276	277 GTGGAGGAGCTTCCCCCCGAGCTTCCGCGAGCCTTCCGGGGCCTTAC 336		ACCGCGGCGGCGGTGGACCG 392	GAACGTCCGGAGGGTCCTCTCCCGCCTCTTCGCCCCGGGAAAGCCCCCAAGGAGAAGGAG 450	ATGCTCACCCGGGACTTCCTGGCCCGCCGCCGCGCGCGCG	CTTTTCGCCCTCGCCCAGGGCCTCCCCCCAGGGCCTGGACCCGGGGGTGTGGAACCAG 510	TGCTGGACGAGATCCTGGGCGGCTGGTGAAGGGGGAGCGGCCGGTCGACCTGGTCGCC 447	GCCCTCATGGAGCTCGGGGCCACGGTCTGCCTGCCGAAACGGCCCCGTTGCGGGGCCTGC 570	GGACTGACGATCCCGGGGCCCTCGCGGGTCATCACCCTGCTCTTCGGCGCCGGTGACGAC 507	571 CCCCTAGGGGCCTTCTGCCGGGGGAAGGAAGGCCCCCGGGGCGTACCCCGCGCCCAGGAAG 630	CGCCGGGAGTTCATCGAGGACCGCAGCGCGGCTCATCGACCGCGGCTACACCCCGGAG 567	CGCCGGGCGAAGGAGGAGCGCCTCGTCGTCCTCGTCCTCGGGCGGAAGGGGGTGCAC 690	CAGGTCGCCAAGGCCCGGGACGAACTCGACGGCTATCTGCGGGAGGTCGACGAGGAGCGG 627		ATCGAGAACCCGGGCACCGACCTGATCAGCCGGCTCGTCATCGACCAGGTGCGGCCGGGG 687	751 GAGCTTCCCGGGCGGGAGGCGGCCTTCGGGGTGAGGTCTAGGCCCCTAGGCGAGGTGCGC 810	CATCTGCGGGTCGAGGATGGTCCCGATGTGCCGGCTGCTGCTGGTGGCCGGTCACGGC 747	811 CACGCCCTCACCCACCGGAGGCTTCGCGTGGAGGTGCGGGGGGCCCTTTGGGAAGGGGAG 870	ACCACCACCAGGCAGCCTGAGCCTGCTCAGCCTGCTCACCGACCCGGAGCTGGCC 807	GGGGAGGACCCCTGGAAGAGGCCCCTACCCAAGCTCATGGAGAAGGTGCTCCGC 924	GGGCGCCTCACCGAGGACCCGGCCCTGCTGCCCAAGGCGGTCGAGGAGCTGCTGCGC 864

Search completed: March 4, 2004, 05:48:50 Job time : 97 secs



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Result
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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975
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11569.813 Million cell updates/sec
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1: geneseqn1980s:*
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ABV72438
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                     Aaa81455 N. mening
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Continuation (11 o
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Ade36257 Human MYH
Aaf21610 Neisseria
Continuation (14 o
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Abz40024 N. gonorr
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Ade36258 Human MYH
Ade36259 Human MYH
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Thermus thermophilus; DNA repair enzyme; enzyme; MutY; RecJ; RecF; TRCF; biochemistry; molecular biology; research; gene; ds.

Thermus thermophilus DNA repair enzyme MutY encoding DNA SEQ ID NO:1.

ABZ22143;

ABZ22143 standard; DNA; 975 BP

12-MAR-2003 (first entry)

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Ada71938	Ab150990	Ab150991	Abq70783	Abq68775	Aax53491	Abn22977	Aac75540	Abq81847	Acf64444	Aas59515	Aax53491	Contin	Adb10743	Adb10741	Adb10739	Acf65382	Continu	Acf69235	Aax34828	Aav37388	Aaz96352
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ALIGNMENTS

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RESULT 1
ABZ21143
IID ABZ22143
XX ABZ22143
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XX 
                                                                        ABZ22143 to ABZ22146 encode the Thermus thermophilus DNA repair enzymes MutY, RecJ, RecF, and TRCF given in ABP56413 to ABP56416. The enzymes cbe used as research reagents for biochemistry and molecular biology
                                                                                                                                                                                                                                                                                                                         A DNA repair enzyme gene, a protein, a recombinant vector, a transformant, preparation of DNA repair enzyme, repairing the error sequence of a DNA, and prevention of error synthesis of a DNA sequence.
                                                                                                                                                                                                                                            Claim 3; Page 13-14; 41pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; ABP56413.
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Sequence 975 BP; 126 A; 347 C;

354 G; 148

T; 0 U; 0 Other;

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                                                                                 GAGGTGCGGGGGGCCCTTTGGGAAGGGGGAGGAGGACCCCTGGAAGAGGCCCCTACCC
                                                                                                                            GCCCCCGGGCGCTACCCCGCGCCCAGGAAGCGCCGGGCGAAGGAGGAGCGCCTCGTCGCC
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                                                             AAGCTCATGGAGAAGGTGCTCCGCAAGGCGCTTCCCCTCCTCGCTCATGCGGGCGTAGTC
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100.0%; Pred. No. 4.5e-160;
tive 0; Mismatches 0;
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129 GCAGGCCCTCCCCTATTACCGCCGCTTTCTGGAGCGCTTTCCCACCCTGAAGGCCCTTGGC 188

GGAGAAGGACCCTTACCGCGTCCTGGTCTCCGAGGTCCTTCTGCAGCAGACCCGGGTGGA 128 GGACAGGCGGGCATATGCTGTGTGGGTCTCAGAGGTCATGCTGCAGCAGACCCCAGGTTGC

327

69

Query Match
Best Local Similarity
Matches 299; Conserv

Conservative

0,

Score 104; DB 9; I Pred. No. 2.6e-09; 0; Mismatches 225;

Length 1608; Indels

30;

Gaps

386

10.7%;

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RESULT 2
ADE36258
ID ADE36258
AC ADE3
XX ADE3
XX Gene

                                                     This invention relates to a novel screening method for identifying an CC individual having a predisposition towards a cancer. Specifically, it CC refers to obtaining a test sample, preferably comprising the hMYH gene that occurs in the base excision repair (BER) pathway, and comparing this CC nucleic acid molecule to the corresponding region of the wild type Sequence. This BER pathway gene, hMYH, acts to protect against G:C to T:A CC transverse mutations in a cancer marker gene such as APC that is seen in CC familial adenomatous polyposis (FAP). As such, mutations identified in CC this may be associated with the onset multiple colorectal adenomas and CC carcinoma. The present invention describes a screening method for CC individuals that works to identify differences comprising any one of CC 382D, Y165C, B466X or Y90X variations in hMYH, this signifies a cancer CC predisposition, particularly for bowel cancer. This polynucleotide Sequence is the mutant G1396T hMYH cDNA that encodes a E466X mutation in CC the encoded polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening, diagnostic and therapeutic methods in individuals with predisposition towards having a cancer, such as colon cancer, usi excision repair pathway or hMYH genes.
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   Sequence 1608 BP; 337 A; 478 C; 502 G; 291 T; 0 U; 0 Other;
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P-PSDB; ADE36261.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; SEQ ID NO 3; 66pp; English.
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/product= "Human MYH
replace(1396,g)
/*tag= b
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ADB367
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ADB37
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ADB37
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ADB37
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BER;
KW Gene
KW Gene
KW BER;
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FT CDS
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FT CDS
FT T CDS
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FT T SAME
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ADB37
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                                                                                                     03-AUG-2001; 2001GB-00018995
                                                                                                                                      02-AUG-2002; 2002WO-GB003591
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WPI; 2003-256601/25
                                                                                                                                                                                                            WO2003014390-A2
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                                                                    UNIV WALES COLLEGE OF
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                                    Cheadle JP;
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                                                                                                                                                                                                                                                                              /product= "Mutant MYH replace(270,c)
                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                             'note= "Base A in the mutant replaces wild type base
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Best Local Similarity
Matches 299; Conserv
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                                                                      GAGCCTGTGCCGGG
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Screening, diagnostic and therapeutic methods in individuals with predisposition towards having a cancer, such as colon cancer, using base excision repair pathway or hMYH genes.
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This invention relates to a novel screening method for identifying an CC individual having a predisposition towards a cancer. Specifically, it refers to obtaining a test sample, preferably comprising the hMYH gene that occurs in the base excision repair (BER) pathway, and comparing this curleic acid molecule to the corresponding region of the wild type sequence. This BER pathway gene, hMYH, acts to protect against G:C to T:A transverse mutations in a cancer marker gene such as APC that is seen in familial adenomatous polyposis (FAP). As such, mutations identified in hMYH are associated with the onset multiple colorectal adenomas and carcinoma. The present invention describes a screening method for individuals that works to identify differences comprising any one of G382D, Y165C, E466X or Y90X variations in hMYH, this signifies a cancer predisposition, particularly for bowel cancer. This polynucleotide sequence is the mutant C270A hMYH CDNA that encodes a Y90X mutation in polypeptide of the invention. G:C to T:A this

Sequence 1608 BP; 338 A; 477 C; 503 G; 290 T; 0 U; 0 Other;

10.7%;

Score 104; DB 9; Pred. No. 2.6e-09;

Length 1608;

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GGAGAAGGACCCTTACCGCGTCCTGGTCTCCGAGGTCCTTCTGCAGCAGACCCGGGGTGGA 128
GGCCTTCTGCCGGG
                                                                                                GGAGCTCGGGGCCACGGTCTGCCTGCCGAAAACGGCCCGTTGCGGGGGCCTGCCCCTAGG 578
                                                                                                                                                 GGGTCTAGCCCAGCAGCTGGACCCAGCCCGGCCAGGAGATTTCAACCAAGCAGCCAT
                                                                                                                                                                                                                                                 GTGCCGTGTCCGAGCCATTGGTGCTGATCCCAGCAGCACCCTTGTTTCCCAGCAGCTCTG
                                                                                                                                                                                                                                                                                                crcccecrrrrcecc--eegaaaeccccaaeeaeaeaecrrrrcecccrceccae
                                                                                                                                                                                                                                                                                                                                                    TGCCTCTATCGCCTTTGGCCAGGCAACCGGTGTGGTGGATGGCAACGTAGCACGGGTGCT
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                                                   GGAGCTAGGGGCCACAGTGTGTACCCCACAGCGCCCACTGTGCAGCCAGTGCCCTGTGGA
                                                                                                                                                                                                eeccrccrcceaeecereeaccce-----
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592
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880

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Query Match
Best Local
                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                            The specification describes a method for determining the risk of a subject to develop cancer. The method comprises determining a level of parameter indicative of a level of activity of a DNA repair/damage preventing enzyme in a tissue of the subject, and determining the risk of the subject to develop the cancer according to the level. The method is useful for determining risk of developing cancer, evaluating effectiveness and dosage of a cancer therapy, and determining the presence of correlation or non-correlation between activity of at least one DNA repair enzyme and a cancer for prevention, early detection and prognosis of cancer. ABV72432-43 encode DNA repair/damage preventing enzymes, whose level or activity may be determined in the method of the
                                                                                                                                                                                                                                                                                                                                 Sequence 1854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determining the risk to develop cancer for prevention, early detection and prognosis, comprises determining a level of parameter indicative of a level of activity of a DNA repair/damage preventing enzyme in a tissue of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 86-87; 91pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the subject.
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09-JUL-2001; 2001US-0303338P.
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                                                                                                                                                                                                                                                                             al Similarity
299; Conserv
TACAGCAGAGAĆĆCTĠĆAGĆAĠCTCĆTĠĊĆŤĠĠCGŤĠĠĠĠĊGCTĀĊĀĊĀĠĀĊŢĠĠĠĠĊCĄŤ
                                                                                                                                                                                      GCAGGCCCTCCCCTATTACCGCCGCTTTCTGGAGCGCTTTCCCCACCCTGAAGGCCCCTGGC 188
                         CCGGCGGCTGCAGGAGGAGC
                                                                             GGAAÇACÇTCÇACCGCCTGGÇCÇĞAAGCGTGGAGGAĞCTTÇCCCCCĞAĞÇTTÇ-----
                                                                                                         CAGTGCTTCCCTGGAGGAGGTGAATCAACTCTGGGCTGGCCTGGGCTACTATTCTCGTGG
                                                                                                                                 CACTGTGATCAACTACTATACCGGATGGATGCAGAAGTGGCCTACACTGCAGGACCTGGC
                                                                                                                                                                                                                 GGACAGGCGGGCATATGCTGTGTGGGTCTCAGAGGTCATGCTGCAGCAGACCCAGGTTGC
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                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                          BP; 397 A; 546 C; 568 G; 343 T; 0 U; 0 Other;
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Pred.
                                                    Mismatches
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No. 2.5e-09;
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밁 Ś 밁 Ś 밁 Ś 밁

Claim 6; Page 37-39;

59pp; English.

cDNA clone codes for human MutY (see AAW31912), which

is homologous

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RESULT 5
AAT 89194
AID AAT 89194
AXX AAT 89194
AXX AAT 8
DT 27-M
DT 27-M
DE Huma
XXX Muty
XXX Muty
XXX Muty
XXX YAT
ET CDS
FT Vari
FT W097
XXX H097
XXX H1-h
XXX H1-h
XXX H9-P;
XXX P-P;
XXX P-
                                                                                                              DNA encoding human Muty protein mismatches in DNA especially in
                                                                                                                                                                                          WPI; 1997-470811/43.
P-PSDB; AAW31912.
                                                                                                                                                                                                                                                                   Wei Y;
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                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human mismatch repair MutY cDNA (hMYH gene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-1998
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                                                                                                    useful for detecting and treating
on-polyposis colon cancer and xeroderma
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC to the Escherichia coli MutY protein involved in the pathway that CC corrects A/G and A/C mismatches as well as adenines paired with 7,8-CC dihydro-8-oxo-deoxyguanine in mutatted DNA. It was isolated from a cDNA CC library derived from human cerebellum tissue. The hMYH gene contains 15 cintrons and is 7.1 kb long. Some naturally occurring allelic variants of CC the coding sequence have been identified. Polynucleotides at least 70% CC and comprising at least 30 nucleotides, can be incorporated into a vector CC and used for production of recombinant polypeptides in host cells. The CC muty polypeptide, or the polynucleotide encoding it, can be used e.g. to creatir oxidative damage to DNA, to prevent mutations from oxidative CC repair oxidative damage to DNA, to prevent mutations from oxidative e.g. CC createrma pigmentosum and neoplasis, and to diagnose an abnormal CC transformation or a susceptibility to abnormal transformation of cells, CC particularly in a non-polyposis colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                    Human cancer
                                                       08-FEB-2001
                                                                                      AAC78090
                                                                                                                          AAC78090 standard; cDNA; 1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1858 BP; 401 A; 546 C;
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                                                                                                                                                                                                                                                                                     GGAGCTAGGGGCCACAGTGTGTACCCCACAGCGCCCACTGTGCAGCCAGTGCCCTGTGGA 1037
                                                                                                                                                                                                                                                                                                                      GGAGCTCGGGGCCACGGTCTGCCTGCCGAAACGGCCCCGTTGCGGGGCCTGCCCCCTAGG 578
                                                                                                                                                                                                                                                                                                                                                                                           GGCCTCCTCCCGAGGGCGTGGACCCG------
                                                                                                                                                                                                                                                                                                                                                                                                                                GTGCCGTGTCCGAGCCATTGGTGCTGATCCCAGCAGCACCCTTGTTTCCCAGCAGCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCCCGCCTCTTCGCCC--GGGAAAGCCCCCAAGGAGAAGGAGCTTTTCGCCCTCGCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGTGCTTCCCTGGAGGAGGTGAATCAACTCTGGGCTGGCCTGGGCTACTATTCTCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGGCCCTCCCCTATTACCGCCGCTTTCTGGAGCGCTTTCCCCACCCTGAAGGCCCTGGC
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                associated gene sequence SEQ ID
                                                     (first entry)
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Pred. No. 2.5e-09;
0; Mismatches 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           567 G;
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                    NO:484
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                                                                                                                                                                                                                                                                                                                                                                                             -GGGGTGTGGAACCAGGCCCTCAT
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                                                                                                                                                                                                                                                                                                                                                                         CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral; CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant; CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant; CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant; CC dermatological; neuroprotectic and antiangiogenic. The conditions or coagulant polypeptides and antiangiogenic. The conditions or coagularing medical conditions and diagnosing pathological conditions. CC polynucleotides, polypeptides, antibodies, apoints and antagonists from cC polynucleotides, polypeptides, antibodies, coagular disorders by activating cc rinhibiting the proliferation, differentiation or mobilisation of cC immune cells, to treat disorders of heematopoietic cells, aucoimmune cC disorders, allergic reactions, graft versus host disease and organ cc rejection, modulate haemostatic or thrombolytic activity, modulate cc inflammation, cancers, cardiovascular disorders, neurological disease and cc agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAA4440 represent sequences used in the exemplification of the argent invention.
                                                                                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiatrheumartic; antiatrhitics; antivixal; antiinflammatory; antithyroid; antiallergic; antibacterial; cardient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 1016-1017; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.
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                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-587533/55
CACTGTGATCAACTACTATACCGGATGGATGCAGAAGTGGCCTACACTGCAGGACCTGGC
                                                                                         GCAGGCCCTCCCCTATTACCGCCGCTTTCTGGAGCGCTTTCCCCACCCTGAAGGCCCTGGC
                                                                                                                                             GGACAGGCGGCATATGCTGTGTGGGTCTCAGAGGTCATGCTGCAGCAGACCCAGGTTGC 568
                                                                                                                                                                                   GGAGAAGGACCCTTACCGCGTCCTGGTCTCCGAGGTCCTTCTGCAGCAGACCCGGGTGGA 128
                                                                                                                                                                                                                                                                                                                     1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruben
                                                                                                                                                                                                                                                                                                                                                                  invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC78448 encode the human cancer associated proteins given
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                   BP; 411 A; 548
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                                                                                                                                                                                                                                                    10.7%;
54.0%;
                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                    Score 104;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                     C; 566
                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                     348 T; 0 U;
                                                                                                                                                                                                                                                      DB 3;
2.5e-09;
                                                                                                                                                                                                                                                                        Length 1878;
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                                                                                                                                                                                                                                                                                                                       5 Other;
                                                                                                                                                                                                                                  30;
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                                                              628
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629

CAGTGCTTCCCTGGAGGAGGTGAATCAACTCTGGGCTGGCCTGGGCTACTATTCTCGTGG

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RESULT 7
AAV35701
ID AAV3
XX AAV3
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XX AAV3
XX AV3
DT 19-A
XX Huma
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  Query Match
Best Local Similarity
                                                                         Sequence 1856 BP;
                                                                                                                  The present sequence encodes human MYH (hMYH). The MYH polypeptide used for diagnosing cancer, where the decreasing levels of the polypeptide are measured in a sample from a patient
                                                                                                                                                                                                                   Claim 6; Page 17-19; 23pp; Japanese.
                                                                                                                                                                                                                                                                                                                   P-PSDB; AAW60243.
                                                                                                                                                                                                                                                                                                                                             WPI; 1998-210407/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-MAR-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV35701 standard; cDNA; 1856
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/product= "hMYH"
                                                                    400 A; 545 C; 568 G; 343 T; 0 U; 0 Other;
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10.5%;
Score 102.6; DB 2;
Pred. No. 4.4e-09;
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                                03-AUG-2001; 2001GB-00018995
                                                      02-AUG-2002;
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                                                                                                                                   /*tag= a "Human MYH mutant protein (Y165C)" replace(494,a) /*tag= b
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Best Local Similarity 53.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid molecule to the corresponding region of the wild type sequence. This BER pathway gene, hMYH, acts to protect against G:C to T:A transverse mutations in a cancer marker gene such as APC that is seen in familial adenomatous polyposis (FAP). As such, mutations identified in hMYH are associated with the onset multiple colorectal adenomas and carrinoma. The present invention describes a screening method for individuals that works to identify differences comprising any one of G382D, Y165C, E466X or Y90X variations in hMYH, this signifies a cancer predisposition, particularly for bowel cancer. This polymucleotide sequence is the mutant A494G hMYH cDNA that encodes a Y165C mutation in the encoded polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1608 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID NO 1; 66pp; English.
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AAGCCCTCCTCGCTGGTACCGGGAAAAACGCCCGCCCCCTCCCCTGGCGGGGGGGAGAAGG 76

Query Match Best Local

Similarity

9.8%;

<u>,</u>

Score 95.6; DB 3; Pred. No. 5.8e-08; 0; Mismatches 224

DB 3;

Length

15,

Gaps

Sequence 349980 BP; 86771 A; 92803 C; 86340 G; 84066 T; 0 U; 0 Other;

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                                                  The present invention describes the full length genome of Neisseria CC meningitidis B (NMB). The sequences in AAP21544 and AAF21607 to AAF21613 CC represent fragments of the NMB genomic sequence, as the sequence was too CC long to go in a record on its own it was split into 8 sequences which CC (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of CC (i.e. the last 49980 bp of AAF21547 are repeated at the beginning of CC AAF21607, the last 49980 bp of AAF21507 are repeated at the beginning of CC Given in AAB5859 to AAF21545 to AAF21588 encode the Neisseria proteins CC grimers which are used in the exemplification of the present invention.

CC The NMB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy. Neisseria nucleic acids, proteins CC and/or antibodies which binds to the proteins can be used in compositions CC diagnostic reagent for detecting the presence of Neisserial bacteria or as a CC diagnostic reagent for detecting the presence of Neisserial bacteria or CC computer storage medium or computer databases can be used in a search to CC identify open reading frames (ORFs) or coding sequences within the NMB CC genome. The DNA sequences provide further opportunities to find antigenic CC outer membrane proteins which are more effective in vaccines than the CC outer membrane proteins currently used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis B full length frames are used to detect, treat and
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The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in other Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GST), examining the array, and determining relative gene expression by an observed hybridisation reporter signal of relative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cell relative to expression of the same genes in one or more second Bacillus cells. The method is useful for monitoring global expression of several genes from a Bacillus cell, discovering new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes
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                                             12-FEB-2001; 2001GB-00003424
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Pred. No. 2.
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Mismatches 183;
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                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                 SEQ ID 4637.
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Matches
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                                               Escherichia
                                                                                              29-JAN-2002
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                                            (strain K-12)
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    CGCCTGGCCCGAAGCGTGGAGGAGCTTCCCCCGAGCTTCG

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                                            A/G-specific adenine glycosylase MutY DNA
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9.5e-07;
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DNA mutation-binding protein; nuclease; DNA

mismatch;

cancer;

PCR

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Sequences AAS63224-AAS63305 represent cDNA encoding and PCR primers used CC chimeric proteins comprising a DNA mutation-binding protein, a linker and CC anuclease, by recombinant technology. The chimeric proteins are useful CC for detection, quantification and mapping of DNA sequence variations including mutations, for example, caused by damage and mismatches. The CC proteins are able to bind to the site of the DNA mutation and cut it out of the molecule. This is useful for early diagnosis of cancer and other CC diseases. The proteins used in the invention include human XFF (or CC (AISEASESE, The proteins used in the invention include human XFF (or CC (AISEASESE, THE PROTEINS USED IN MINISTER (AISEASE), buman xeroderma pigmentosum complementation groups A, C and E (CC (XPA, XPC and XPE), human Muts homologue 2 (hMSH2), Serratia marcescens CC (MSH2), Thermus thermophilus Muts, Escherichia coli Fapy-DNA CC glycosylase (Muty), synthetic T4 endonuclease V (T4 endo V), thymine DNA-CC (Slycosylase (TDG), E. coli Uvr A, B and C, and E. coli endonucleases and
                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant chimeric protein, useful for detecting and quantifying mutations, e.g. in disease diagnosis, comprises mutation-binding pi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mc Cutchen- Maloney
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29-AUG-2000;
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2000US-00650855.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           547 T; 0 U; 0 Other;
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                                                                                                                                     CC The present invention describes a method for predicting the epidemic CC character of a Mycobacterium tuberculosis isolate and/or a selective CC advantage to be maintained in the host and/or the acquisition of multiple CC drug resistance (MDR) by the isolate comprising detecting an alteration of the DNA repair system of the isolate. Also described: (1) detecting a CC Mycobacterium tuberculosis strain with a MDR phenotype; (2) a CC polynucleotide; (3) a kit for detecting Mycobacterium tuberculosis; (4) an Escherichia coli strain containing the plasmid pMYC2501; and (5) CC detecting in a patient infected by Mycobacterium tuberculosis a higher CC risk of being unable to eliminate the bacillus or of developing MDR CC riberculosis. The method is useful for predicting the epidemic character CC of a Mycobacterium tuberculosis isolate and/or a selective advantage to be maintained in the host and/or the acquisition of MDR by the isolate. CC The present sequence represents a M. tuberculosis muty open reading frame companies.
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21-AUG-2001;
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Pred. No. 2.7e-06;
0; Mismatches 309
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ID ABZ79955
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AC ABZ79
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XX I19-MA
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XX Mycob
KW Mycob
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21-AUG-2001;
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Query Match Best Local S

8.9%; A; 471

Sequence

1312

BP; 173

U; 0 Other; Length 1312;

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Predicting the epidemic character of a Mycobacterium tuberculosis isolate and/or the acquisition of multiple drug resistance (MDR) by the isolate by detecting an alteration in the DNA repair system of the isolate.
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                                                                                                                                              Disclosure;
                                                                                                                                                                                              WPI; 2003-256711/25
                                                                                                                                             Fig 6A; 83pp; English
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The present invention describes a method for predicting the epidemic CC character of a Mycobacterium tuberculosis isolate and/or a selective advantage to be maintained in the host and/or the acquisition of multiple CC drug resistance (MDR) by the isolate comprising detecting an alteration in the DNA repair system of the isolate comprising detecting an alteration CC Mycobacterium tuberculosis strain with a MDR phenotype; (2) a CC polynucleotide; (3) a kit for detecting Mycobacterium tuberculosis; (4) and Escherichia coli strain containing the plasmid pMYC2501; and (5) CC detecting in a patient infected by Mycobacterium tuberculosis a higher CC risk of being unable to eliminate the bacillus or of developing MDR CC tuberculosis. The method is useful for predicting the epidemic character CC of a Mycobacterium tuberculosis isolate and/or a selective advantage to be maintained in the host and/or the acquisition of MDR by the isolate. CC The present sequence represents a M. tuberculosis muty nucleotide and/or the exemplification of the present invention or the present invention of the present invention or the present invention of the present invention or the present in the present in C; 457 G; 211 T; 0

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Pred. No. is the number of results predicted by chance to have

REFERENCE AUTHORS TITLE

1 (bases 1 to 975)
Kuramitsu, N. and Yokoyama, S.
Kuramitsu, N. and Yokoyama, S.
DNA restoration enzyme gene
Patent: JP 2002247985-A 1 03-SEP-2002;

JOURNAL

Thermus.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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OS Thermus thermophilus
PN JP 2002247985-A/1
PD J3-SEP-2001 JP 2001047762
PF 23-FEB-2001 JP 2001047762
PC C12N15/09,C07K14/195,C12N1/15,C12N1/19,C12N1/21,C12N5/10
PC C12N15/09,C07K14/195,C12N1/15,C12N1/19,C12N1/21,C12N5/10
PC C12N9/14,C12N9/16,
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Local Similarity 58.4%;
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partial cds.
AF377342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1089)
Li,X. and Lu,A.-L.
Direct Submission
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Deinococcus radiodurans R1
Bacteria; Deinococcus-Thermus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deinococcus radiodurans
J. Bacteriol. 183 (21),
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                                                                                                 /transT_table=11
/transT_table=11
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/strain="R1"
                                                                                 LDHKALDVWRQRQAGLFGAALDSSPLGEA"
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                                                                                                                                                                l (bases 1 to 11378)
white,O., Eisen,J.A., Heidelberg,J.F., Hickey,E.K., Peterson,J.D. Dodson,R.J., Haft,D.H., Gwinn,M.L., Nelson,M.C., Richardson,D.L. Moffat,K.S., Qin,H., Jiang,L., Pamphile,W., Crosby,M., Shen,M., Vamathevan,J.J., Lam,P., McDonald,L., Utterback,T., Zalewski,C., Makarova,K.S., Aravind,L., Daly,M.J., Fraser,C.M. et al. Genome sequence of the radioresistant bacterium Deinococcus
White,O., Eisen,J.A., Heidelberg,J.F., Hickey,E.K., Peterson Dodson,R.J., Haft,D.H., Gwinn,M.L., Nelson,W.C., Richardson, Moffat,K.S., Qin,H., Jiang,L., Pamphile,W., Crosby,M., Shen,
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Deinococcus radiodurans R1
Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
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Makarova, K.S., Aravind, L., Daly, M.J., Minton, K.W.,
Fleischmann, R.D., Ketchum, K.A., Nelson, K.E., Salzberg,
Smith, H.O., Venter, J.C. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (08-NOV-1999) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                CYCLAHRCRRTLEVWILKVRSEFKPSGDQPTA I ASL VDGLESGLRYQTLLGATGTKY
YSMAKVI EEVQRALLMAPKI LTAQLASEFREF PDAA VEFT IS YYDY YQFEA YVPG
YSMAKVI EEVQRALLMAPKI LTAQLASEFREF PDAA VEFT IS YYDY YQFEA YVPG
KDLFI IEKDASVNQE IERLHSTTRSLLTRROTI VVASVSCI YGLGDRYEYTALMA IVK
KGGVMPRDELLGRLVNMQYERND I ELMPGRFS VKGETVTWPAY DEQPLR I ELMGDDV
ER I SVUHPLTGERLGDLDATVVY PAKHYVSSAGNI ERAI GS. 1006LDBRLEY FHISVGK
LLEAQRLKERTLYDLEMLKVLGY CSGI ENYSRH I DGRAPGAT PYTMLDY FPDDF ITFI
DESHVTVPQ I GGMANGDRARKGTLNVGTSRLSSAMDURPLNFEEFLSKTGQTVEVSAT
DESHVTVPQ I GGMANGDRARKGTLUVGFFTI FP I QGD I EDLLGRVERTAAGERTLVTTL
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EEVSLVAI LDADKFGFTRASDRALI QTI GRARANVNGEVI LYADVVTPAMR FAMDETAR
RREKQLAYNEBHGI TPRTVI GGVRDVI RGEBLLEGE I SSENVSGDRDSLTAQLTDLELD
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complement (3287. .4006)

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identity: 51.02; identified by sequence similarit
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                                                                                                                                                                                                                                                                                        note="identified
                                                                                                                                                                                                                                                                                                             'gene="DR2276"
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complement (3993. .4811)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to SP:P45465 PID:606088 GB:U00096 PID:1789538 percent identity: 56.57; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="DR2282"
8243. .8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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/db_xref="GI-6460094"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVLTIEGEADTGELRILAVEG"
complement (8625. .9431)
/gene="DR2283"
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/gene="DR2282"
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vsrepggtlvftevrqrrqarygsaldsvtprklalmhraaleyltrecgrddlpcrl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="DR2283"
/note="similar to SP:Q55282 percent identity:
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Pred. No. 9.1e-15;
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AF543480
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PUBMED
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Read bacterium plasmid pAK106 SodA (sodA) gene, partial concert (greA), MutY (mutY), putative aminopeptidase, and putative response regulator genes, complete cds; and unknown genes.

AF543480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (06-SEP-2002) Institut f. Mikrobiologie, University of Goettingen, Grisebachstr. 8, Goettingen D-37077, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 8249)
Knietsch, A. and Daniel, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Knietsch,A., Waschkowitz,T., Bowien,S., Henne,A. and Daniel,R. Construction and Screening of Metagenomic Libraries Derived from Enrichment Cultures: Generation of a Gene Bank for Genes Conferring Alcohol Oxidoreductase Activity on Escherichia coli Appl. Environ. Microbiol. 69 (3), 1408-1416 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uncultured bacterium uncultured bacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; environmental samples.
1 (bases 1 to 8249)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCGGTGGCCCTCCTGATCGGGGACGCCGAGTACGCCGTGCTGGAAAAGCGGGAGGGCTC 10509
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                                                                                                                                                                                                                                                                                                                              complement (673. .2466)
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                                                                                                                                                                                                                                                                                                                                                                             /product "soda"
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/protein_id="AAO59964.1"
/db_xref="Gil:28875483"
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VLDLMEHAYMDDFGPKGRGAYSKFILENTDMEVVEARFARARNGA"
                          LRPORTFYGGPREVVAKTECSGOHPFDYALEDGHPLAEABRGGOGGGGAPDTGORGO
LAAARELAAMLHHRLIKTAVQVARAAVVAQAA BEREHYVQQRRRGGRLHVGKTLQEPGV
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                                                                                                                           /product="GreA"
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                                                                                                                                                                                                                                                                                                         complement (673. .2466)
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                                                                                                                                                                                                        /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transI_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene='
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /environmental_sample
/plasmid="pAK106"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/isolation_source="soil"
/db_xref="taxon:77133"
                                                                                                                                                                                                                                                                            'gene="greA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="sodA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="anonymous microbial sequence conferring formation of carbonyls from short-chain polyols on Escherichia coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="uncultured bacterium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                       note="putative transcription factor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="putative superoxide dismutase"
                                                                                                 translation="MRHADGLQGAGSALRPAQGADAGAQVHQALRVGRDALRGQQGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       720
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complement (6591.

note="Orf10; hypothetical

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RRTRVPVRPTARA"

note="Orf9"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="putative a
/codon_start=1
/transl_table=11
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ADPRTFHWTGPAPLFTELDDADSDTRVGTPRPGARGRVVSSALVRDAGGTAETTTP
PARNEPARGYMTAAGAERTYRRELQQL/VQRRDELLASPDDDLPERSELATLERELAQVSTA
VLQGAIVIRLASPPRDEVRFGAEVVVEDDRGSRSRFQLVGENEAAPERGLVNWFSPLG
                                                                                                                                                                                                                                              ARRRSMARLRTCQQPGHRPCDREKQAPERGFLVVGPARGAPAGEWVRCRSRWHSRRRA
WPASWSRSGPRVPRPCRSRLRRPPWRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="mkrtlftlaiaalsaigsagvfaqttdtggllrdkagktlylfd
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kvgdtsgdosggvwhvikaaggdkfgekraatgnaadfyky"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFPRSSEMLATLPGIGRSTAAAIAAFCFGERVÄILDGNVKRVLTRALGFGDDLSRPAN
ERALWAQAQTTLLPAQGITAYTQGLMDLGAGICTLRRPQCAACPLQPVCVAHAQGRPEA
YPVKTRRLKRGQRANVVLWLVHGLQVWLVRRPEQGVWAGLWSLPEWPADDSLGTLAAA
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/db_xref="GI:28875488"
                                                                                                                                                                                                           complement (5521. .5868)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (2904.
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/gene="mutY"
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transl_table=11
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'transl_table=11
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                                                                                                                                                                               note="Orf8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="Orf6; hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="Orf7; hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adenine glycosylase"
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Query Match
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/db_xref="G1:28875491"
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RQHGRREPVAATPGSEPSSHQPQAPDAQASGEPRAAEVHPAGGPDADDETDRRRPLAVP
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TITLE
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The complete genome sequence of Chromobacterium violaceum reveals
remarkable and exploitable bacterial adaptability
Proc. Natl. Acad. Sci. U.S.A. 100 (20), 11660-11665 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chromobacterium violaceum ATCC 12472
Chromobacterium violaceum ATCC 12472
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Chromobacterium.
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                                                                                                                                                                                                                                                                                                                            gene="rplI"
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ATCC 12472 section 14 of 16 of the
                                                            ...al protein .
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                                                                                                                                                                                                                                                                                                                                                                                                                              /locus tag="CV3641"
complement(1631. 1927)
/locus tag="CV3641"
/codon_mr="CV3641"
                                                                                                                                                     complement (1984...2307)
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complement (1984. . 2307)
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GMIESDRYCVDVLTQVAAVKSALDAVALQLLENHMKGCVARALQQGDATGMVTELIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKDEKAKNLLDAQPAAEVEASA"
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RQLAYPIQKLHKAHYVLMNVECQAETLAEIEHAFKFNDAVLRHLTIKMDRAISDASPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (1100. .1474)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /locus_tag="CV3639" complement(782. .1081)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="marqlfkrkkkfcrftaegikeidyksvollkofiaengkiipar
itgtkaryqrqlttaikrarflafleytoqh"
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/translation="MQNRLVLTVTVDREDALRYTPAGLPVVEMWLKHQSRQSAGGFER
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/trans[_table=
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TATTACCGCCGCTTTCTGGAGCGCCTTTCCCACCCTGAAGGCCCTGGCCGCGGCTTCCCTG
                                                                                               TATCGGGTGTGGCTGTCAGAGAGTCATGCTGCAGCAGACCCAGGTGAAGAGCGTGCTCGAC 66821
                                                                                                                                                   TACCGCGTCCTGGTCTCCGAGGTCCTTCTGCAGCAGACCCGGGTGGAGCAGGCCCTCCCC 141
                                                                                                                                                                                                                 CTGGTGGCCTGGCAACGGCGCATGGCCGCCACGACCTGCCCTGGCAGGTGAAGGACCCCG 66881
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dosyldoylcmlkdviaktagyrrecaasldlcnvacgrtegffelmlkfwdiaagsl
ivqeaggiytdptgeggwfesgdivagnpkvlaqllqllaphvak"
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Aplpaaaalglargloldikrlplerkogalargcitaaavslplicpokpateemayn

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AWRDVVNVPPGQXVALRFRQDMPGPRMFHCHILEHEDAGMMGTLDVRA"
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/trans1_table=11
/product="grobable RNA methyltransferase"
/protein_id="AAQ61307.1"
/db_xrefe"GI:34104951"
/db_xrefe"GI:34104951"
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/note="identified by sequence similarity; putative; ORF
located using Glimmer/GeneMark/Blastx/COG0483"
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/note="identified by sequence similarity; putative;
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;736. .6581
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|protein id="AAQ61305.1"
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                                                                           Salanoubat,M., Genin,S., Artiguenave,F., Gouzy,J., Mangenot,S., Arlat,M., Billault,A., Brottier,F., Camus,J.C., Cattobico,L., Chandlar,M., Choisne,N., Claudel-Renard,C., Cunnac,S., Demange,N., Gaspin,C., Lavie,M., Moisan,A., Robert,C., Saurii,W., Schiex,T., Siguier,F., Thebault,F., Whalen,M., Wincker,P., Levy,M.,
           Weissenbach, J. and Boucher, C.A.
Genome sequence of the plant pathogen Ralstonia
Nature 415 (6871), 497-502 (2002)
                                                                                                                                                                                                                                                                             Ralstonia solanacearum
Ralstonia solanacearum
Bacteria; Proteobacteria; Betaproteobacteria;
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AL646059.1 GI:17427391
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                                                                                                                                                                                                                                                              Burkholderiaceae; Ralstonia.
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Gene name confidence: hypothetical
predicted by Homology
predicted by FrameD"
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Gene name confidence: hypothetical
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predicted by Homology
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                                                                                                                                                                                                                                                                                                                                                                                        codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="RSc0383"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Product confidence: putative Gene name confidence: putative predicted by Codon_usage predicted by Homology predicted by FrameD"
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Gene name confidence : hypothetical
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predicted by Homology
predicted by FrameD"
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GRLPTQLHLMEELKKVRRVIGKAMATAPHETLLVIDANTGQNALAQVKAFDDALGLTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="synonyms: RS03354, complement(2924. .3910)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (2924. .3910)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAMCASILWFSLLGFGARLLEPVFARPVAWRVLDALIGAVMWAIALTLLMGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YVLGVVLICALCDMALIALGVAGMGTLISAHPAWLTAVRWAGAAFLLAYGARAFRAAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="ftsY"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="synonym: RS03353"
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Matches 322;
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CGTGGACCCGGGGGTGTGGAACCAGGCCCTCATGGAGCTCGGGGGCCACGGTCTGCCCTGCC 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCCTGGGCGGGCCTGGGCTACTACACCCGCGCGCGCAATCTGCACCGCTGCGCGCAGAT 19240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCGGAGATCATGCTGCAGCAGACGCAGGTGTCGGCGGTGCTGGGCTACTACGCCCGCTT 19120
                                                                             CGGCGACAAGCGCGTCGAGGAAACGATGTGGCCGCATCGCCGAGACCGTGCTGCCCCCGGC 19480
                                                                                                                         CCGGGAAAGCCCCAAGGAGAAGGAGCTTTTCGCCCTCGCCCAGGGCCTCCTCCCCGAGGG 485
                                                                                                                                                                               CATCCTCGACGGCAACGTCAAGCGCGTGTTTGCGCGCGTCTTCGGCATCGACGGCTTTCC
                                                                                                                                                                                                                           GGCGGTGGACGGAACGTCCGGAGGGTCCTCTCCCCGCCTCTTCG------C
                                                                                                                                                                                                                                                                            TGGTCTCGGGCCTTACACCGCGGCGGCGGTGGCCTCCATCGCCTTCGGGGAGCGGGTGGC 380
                                                                                                                                                                                                                                                                                                                                                                            CGTGGTGGCCGAGCATGGCGTGCGTTTCCGCGCGATCCCGAGGCGCTGGCGGCGCGCTGCC 19300
                                                                                                                                                                                                                                                                                                                                                                                                                               CGTGGAG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTGGAGCGCTTTCCCACCCTGAAGGCCCTGGCCGCGGCTTCCCCTGGAAGAGGTCCTTAG 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGCCACGGCCGCCATCACCTGCCGTGGCAGAACACCGGTGACGCCTATCGCGTGTGGCT 19060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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REDILLVKGKDEKGGRLADDVNAGYDGMNRGPSIFLLDGVPALGHTTAETEQALRAQI
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KSVTPAQVQQVAKTYFTEDNLVVATLLPQPIDPNKPARKPVPGMREEGGLR"
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/EC_number="3.4.99.-"
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629. .6972
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1124. .5629
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transl_table=11
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57.0%;
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Pred. No. 7.4e-11;
0; Mismatches 213;
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/locus tag="BP3611" /note="Similar to Becherichia coli elongation factor Tu /note="Similar to Becherichia coli elongation factor Tu /note="Similar to Becherichia coli elongation factor	/gene=" /locus /note=- 7612 /gene='	P "C	AUTHORS Sebainia, M. TITLE Direct Submission JOURNAL Submitted (06-AUG-2003) Submitted on behalf of the Pathogen Sequencing Unit, Sanger Institute, Wellcome Trust Genome Campus, Sequencing Unit, Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A, E-mail: ms5@sanger.ac.uk	Comparative analysis of the genome organic pertussis, Bordetella parapertussis and Bordetel Online Publication Nat. Genet. DOI:10.1038/Ng1227-10.1038/Ng1227 2 (bases 1 to 257701)	REFERENCE AUTHORS Parkhill, J., Sebaihia, M., Preston, A., Murphy, L.D., Thomson, N., Harris, D.B., Holden, M.T.G., Churcher, C.R., Bentley, S.D., Mungall, K.L., Cerdeno-Tarraga, A.M., Temple, L., James, K., Harris, B., Quail, M.A., Achtman, M., Atkin, R., Baker, S., Basham, D., Bason, N., Cherevach, I., Chillingworth, T., Collins, M., Cronin, A., Davis, P., Doggett, J., Feltwell, T., Goble, A., Hamlin, N., Hauser, H., Holroyd, S., Jagels, K., Leather, S., Moule, S., Norberczak, H., O'Neil, S., Ormond, D., Price, C., Rabbinowitsch, E., Rutter, S., Sanders, M., Saunders, D., Seeger, K., Sharp, S., Simmonds, M., Skelton, J., Squares, R., Squares, S., Stevens, K., Unwin, L., Skelton, J., Squares, R., Squares, S., Stevens, K., Unwin, L., Whitehead, S., Barrell, B.G. and Maskell, D.J.	-	RESULT 7 BX640422 BX640422 BX640422 BX640422 BX640422 BX640422 BX640422 12/12	Db 19481 GGACGGCATCCAGTCGTACACGCCAGGGCCTGATGGACCTGGGCGCCACGGTCTGCACGCG 19540 Qy 546 GAAACGGCCCGGTTGCGGGGCCTGC 570
misc_feature	CDS	misc_feature	misc_feature		CDS	gene	misc_feature misc_feature	, ¹ ⊨n
/note="Similar to Escherichia Coli and Indee Similar to Escherichia Coli and Indee Scores: EX I3 RPIC SW:RLJ ESCOLI (P02386) (209 aa) fasta scores: EX 8.6e-48, 67.77% id in 211 aa, and to Neisseria 8.6e-48, 67.77% id in 211 aa, and to Neisseria 8.6e-48, 67.77% id in 211 aa, and to Neisseria 9.69 klasticis 50s ribosomal protein L3 MAA0129 TR:Q9JRH6 (EMBL:AL162752) (214 aa) fasta scores: E(): 2.4e-51, 69.48% id in 213 aa" /codon start=1 /transI_table=11 /transI_table=11 /product="S0s ribosomal protein L3" /product="S0s ribosomal protein L3" /protein id="CAB43871.1" /protein id="CAB43871.1" /db_xref="G1:33564555" /translation="MGRKVGMTRIFTEDGESIPVTVLDVSNNRVTQVKSLESDG9* /formarkation="MGRKVGMTRIFTEDGESIPVTVLDVSNNRVTQVKSLESDG9* /translation="MGRKVGMTRIFTEDGESIPVTVLDVSNNRVTQVKSLESDG9* /formarkation="MGRKVGMTRIFTEDGESIPVTVLDVSNNRVTQVKSLESDG9* /formarkation="MGRKVGMTRIFTEDGESIPVTVLDVSNNRVTQVKSLESDG9* /formarkation="MGRKVGMTRIFTEDGESIPVTVLDVSNNRVTQVKSLESDG9* /formarkation="MGRKVGMTRIFTEDGESIPVTVLDVSNNRVTQVKSLESDG9* /formarkation="MGRKVGMTRIFTEDGESIPVTVLDVSNNRVTQVKSLESDG	/gene="rplC" /locus_tag="BP3613" 2044.	14141461 /gene="rpsJ" /gene="rpsJ" /locus tag="BB3612" /note="GcanRegExp hit to PS00361, Ribosomal protein S10 /note="GcanRegExp hit to PS00361, Ribosomal protein S10 signature. Confirmed by InterPro eMOTIF pattern match." 20442688	Q" 13421629 /gene="rpsJ" /locus tag="Bp3612" /note="HMMPfam hit to PF00338, Ribosomal protein S10p/S20e"	roduct="305 LLDOSMIL FRODUCT rotein id="CRE38870.1" b xref="GI:33564554" b xref="GI:33564554" ranslation="MKNQKIRIRLKAFDYKL: raydvlrsphynkTsrdQFEIRTHQRLMD'	/3001641 /gene="rps0" /locus tag="BB9612" /locus tag="BB9612" /locus tag="BB9612" /note="Similar to Escherichia coli 30S ribosomal protein /note="Similar to Escherichia (103 aa) fasta scores: S10 Rps0 SW:RS10 ECCLI (P02364) (103 aa) fasta scores: E(): 8 46-28, 76-47\$ id in 102 aa, and to Neisseria meningitidis 30S ribosomal protein S10 NWA0133 TR:Q9JR21 (EMBL;AL162752) (103 aa) fasta scores: E(): 1.2e-29, 79.61\$ id in 103 aa" /codon start=1 /transl_table=11 /transl_table=11 /transl_table=11	/locus_tag="BP3611" /note="ScanRegExp hit to PS00301, GTP-binding elongation / notes signature. Confirmed by InterPro eMOTIF pattern match." 1301641 /gene="rpsJ" /locus_tag="BP3612" /locus_tag="BP3612"	/gene="tuf" /gene="tuf" /locus tag="BP3611" /locus tag="BP3611" /note="ScanRegExp hit to PS00017, ATP/GTP-binding site /mottf A (P-loop)." 226 273 226 273	KIIK" 1031203 /gene="tuf" /locus_tag="BP3611" /note="HMMPfam hit to PF00009, Elongation factor Tu /notesity"

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Best Local
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  CTCCGAGGTCCTTCTGCAGCAGACCCGGGTGGAGCAGGCCCTCCCCTATTACCGCCGCTT 155
                                         CCGCCACGGCCACGATCTGCCCTGGCAGAACACCCGCGACCCCTATCGCATCTGGCT 217892
                                                                               CCGGGAAAAACGCCCGCCCCCCCCCCCGGCGGGGGGAAAGAACCCCTTACCGCGTCCTGGT 95
                                                                                                                      Conservative
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/locus_tig="Bp3615"
/note="Similar to Escherichia coli 50S ribosomal protein
/note="Similar to Escherichia (100 aa) fasta scores:
L23 Rplw Sw:RL23_ECOLI (P02424) (100 aa) fasta scores:
E(): 1.5e-14, 54.94% id in 91 aa, and to Neisseria
meningitidis 50S ribosomal protein L23 NMA0127 TR:09JX11
(EMBL:AL162752) (106 aa) fasta scores: E(): 6.9e-19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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GNRAQKDRAEVKHSTKKPWRQKGTGRARAGMTSSPLWRGGGRAFPNSPEENFSQKVNK
KMYRAGIRSILSQLAREDRVAVDTFTLESPKYKLAAAKLKSLGLDSVLIITDNVDEN
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/note="Similar to Escherichia coli 50S ribosomal protein
/note="Similar to Escherichia coli 50S ribosomal protein
L4 RplD SW:RL4 ECOLI (P02388) (201 aa) fasta scores: E():
5.9e-41, 58.33$ id in 204 aa, and to Neisseria
meningitidis 50S ribosomal protein L4 NMA0128 TR:Q9JRA2
(EMBL:AL162752) (206 aa) fasta scores: E(): 2.4e-51,
65.02$ id in 203 aa"
                                                                                                                                                                                                 /locus tags BP3616"
/locus tags BP3616"
/notes Similar to Escherichia coli 50S ribosomal protein rotes RplB SW RLL ECOLI (P02387) (272 aa) fasta scores: E(): 2.4e-75, 67.03 id in 273 aa, and to Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mnaerlmqvilapivtekatfvaeknqqvafrvvadatkpeika
avellfkvqvesvqvlnrkgkvkrfgrfvgrrrnerkayvalkdgqeidfaevk"
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2693. .331
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/locus_tag="BP3613"
/note="ScanRegExp hit to PS00474, Ribosomal protein L3
                                                                                                                                                                                                                                                                                                                                                                                                                     gene="rplw"
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                                                                                                                                                                                                                                                                                                                                        gene="rplB"
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note="HMMPfam hit
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604. .4431
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Pred. No. 1.1e-09;
0; Mismatches 150;
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                                                                                                                                                       Length 257701;
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218193 CATCATGGÁCGGCAACGTCAAGCGGGTGTTCACGCGCCACTTCGGCATCGÁGGGC 218247
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Harris,D.E., Holden,M.T.G., Churcher,C.R., Bentley,S.D.,
Mungall,K.L., Cerdeno-Tarraga,A.M., Temple,L., James,K., Harris,B.,
Quail,M.A., Achtman,M., Atkin,R., Baker,S., Basham,D., Bason,N.,
Cherevach,I., Chillingworth,T., Collins,M., Cronin,A., Davis,P.,
Doggett,J., Feltwell,T., Goble,A., Hamlin,N., Hauser,H.,
Holroyd,S., Jagels,K., Leather,S., Moule,S., Norberczak,H.,
O'Neil,S., Ormond,D., Price,C., Rabbinowitsch,E., Rutter,S.,
Sanders,M., Saunders,D., Seeger,K., Sharp,S., Simmonds,M.,
Skelton,J., Squares,R., Squares,S., Stevens,K., Unwin,L.,
Whitehead,S., Barrell,B.G. and Maskell,D.J.
Comparative analysis of the genome sequences of Bordetella
pertussis, Bordetella parapertussis and Bordetella bronchiseptica
Online Publication
Nat. Genet. DOI:10.1038/Ng1227-10.1038/Ng1227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (06-AUG-2003) Submitted on behalf of the Pathogen Sequencing Unit, Sanger Institute, Wellcome Trust Genome Car Hinxton, Cambridge CB10 ISA, E-mail: ms5@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete genome.
Bordetella parapertussis
Bordetella parapertussis
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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BX640435.1 GI:33574489
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Bordetella parapertussis strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATCATGCAGCGCTGCGTCGGCCGCTTTCCCCCCGCGCGCCGAAGAGATCGCCACCCTGCC 218132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCGGAAATCATGCTGCAGCAGACGCAGGTGGCGACGGTCATTCCGTATTACCAGCGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCGGTGGACGGGAACGTCCGGAGGGTCCTCTCCCGCCTCTTCGCCCGGGAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGCATCGGCCGCTCCACGGCCGCCGCCATCGCCGCCTTCGCCTACGGCGAGCGCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTGGCCCGAAGCGTGGAGGAGCTTCCCCCGAGCTTCGCCGAGCTTCGGGGGCTTCC
                                                                                                                                                         /locus_tag="BPP3852"
complement(293. .937)
/note="ortholog of Bordetella pertussis (BX470248) BP3166"
/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                          complement(293. .937)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                           gene="ureG"
                                                                                                                                                                                                                       gene≃"ureG"
                                                                                                                                                                                                                                                                                                                        strain="12822"
                                                                                                                                                                                                                                                                                                                                                                                organism="Bordetella
                                                                                                                                                                                                                                                                                        xref="taxon:519"
                                                                                                                                                                                                                                                                                                                        _type="genomic DNA"
_in="12822"
                                                                                              _tag="BPP3852"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12822,
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complete ge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217952
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CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
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DYALAQAAYHAHEAHPHAHSHAGGHGHVHSGHGHGKHGEHDAES"
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complement(2267. .3982)
                                                                                                                                                                                                                                                                                                                                complement (2267. .3982)
cranslation="MTRISRSAYAEIYGPTVVGGVGDRVRLADTLLLAEVEKDHTIFG
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/RC_number="3.5.1.5"
/note="crtholog of Bordetella pertussis (BX470248) BP3168"
                                                                                                                                                                                                                                 'gene="ureC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (1944. .2249)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /locus_tag="BPP3853"
/note="HMMPfam hit to PF01730,
complement(1647. .2264)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(1094. .1546)
/gene="uref"
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PLGQWAGQRWLERLRAGIFAVLADARARAGATFPRLDTFAPQYALVSARHETQFSRLF
                                                                                                                                                                                                                                                                                                                 gene="ureC"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="ureE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP3167A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (1647. .2264)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="urease accessory protein"
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GPPDADIVFVESGGDNLAATFSPELSDLTLYIIDVASGEKIPRKGGPGITKSDLFIIN
KTDLAPYVGADLAVMEADTRRMRGDKPFVMCNLKTGDGLDQVIAFLKTEGLFRG"
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| Mote=_rrtholog of Bordetella pertussis (BX470248)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /locus_tag="BPP3852"
/note="PS00017 ATP/GTP-binding
complement(962. .1624)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /locus_tag="BPP3852"
/note="HMMPfam hit to PF01495,
nucleotide-binding domain, sco
complement (848. .871)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (962. .1624)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        locus_tag="BPP3854"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1/transI_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="ureF"
/locus_tag="BPP3853"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (509. .892)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="ortholog of Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="ureF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="ureG"
                                                                                                                                    start=1
                                                                                                       _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _tag="BPP3853"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               495, HypB/UreG
score 4.5e-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UreF, score 9.7e-74"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           site motif A (P-loop)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BX470248) BP3167"
                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
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/locus tag="BPP3857"
/locus tag="BPP3857"
/note="Signal peptide predicted for BPP3857 by Signalp
HMM (Signal peptide probabilty 1.000) with cleavage sit
probability 1.000 between residues 26 and 27;
                                                                                                                                                                           / LTAINS I ALL ON "MICAMSKRAMLGSGAAALMLFSGAALAHPGHLGHELPGSMFAAGF WHPLTGFDHLLAMLAVGMWSALTHHTARQAVWLPVMFLALLFRGAMMGMAGVRLDAVE PVIMVSLLVLGLLVASRKAVQGWAGFALVGGFALLFHGLAHGMELPGSEGALGFVAGFM LATLGLHLAGJFAGFRLKHMNILWLSRALGVGI AGYGALLFVGARV"
                                                                                                                                                        complement (4844.
                                                                                                                                                                                                                                                                                                  /codon_start=1
/transI_table=11
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/protein_id="CAE39140.1"
/db_xref="G1:33574495"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l aa and was clipped.

HMMPfam hit to PF00699, Urease beta subunit, score 3.2e-60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/trans1_table=11
/trans1_table=11
/product="urease beta subunit"
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/krans1ation="MIPGEINTERGNAVRFEPGMRRTVELVAVGGERRIFGFQGKVMGALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /locus_tag="BPP3857"
complement(4304. .4921)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (3985. .4284)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (4304. .4921)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /locus_tag="BPP3856"
complement(3979. .4287)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EBVKFGGGKVIRDGMGOSQRLATDCVDTVITNALIIDAVTGIVKADIGIKDGLISGIG
KAGNPDYQGGVTIIIGASTEVVAGEGLIVTAGAIDTHIHFICPQQIEBALATGTTTMI
GGGTGBATGSLATTSTSGEMHMAAMLQALDAFPVNVGLFGKGSSSSHGALLEQVRAGA
MGLKIHEDWASTPASIDTCLNVAEETDIQVAIHSDTLNESGFVEDTFAAKKGRTIHSF
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LAFAESRIRRETIAASDILHDLGAFSIMSSDSQAMGRVGETVLRTWQTAHKMKLQRGP
LQGDSERSDNERIKRYIAKYTINPAVAHGIAHLVGSVEVGKLADLVLWKPAFFGVKVN
MVLKSGMAVSASIGDMGASISTPQPVQIRPMMGSHGKALRTSVAFVSQVSLSNPAVSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 locus_tag="BPP3857"
/note="ortholog of Bordetella pertussis (BX470248) BP3170"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="ureJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /locus_tag="BPP3856"
/note="This hit extended beyond the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (3979. .4287)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /locus_tag="BPP3855"
/note="HMMPfam hit to PF00449, Urease alpha-subunit,
N-terminal domain, score 4.8e-83"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        catalytic domain, score 0" complement (2969. .3019)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="ureJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="ureB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (3584. .3979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /locus_tag="BPP3855"
/note="P801120 Urease nickel ligands signature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (3548. .3589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (2273. .3580)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RYFLF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EC_number="3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /locus_tag="BPP3855"
/note="PS00145 Urease active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EC_number="3.5.1.5"
note="ortholog of Bordetella pertussis (BX470248) BP3169"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /locus_tag="BPP3855"
/note="HMMPfam hit to PF02802, Urease alpha-subunit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="ureB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="ureC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="ureC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        locus_tag="BPP3856"
                                                                                                                                                           .4921)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   end of the feature
                               alp 2.0
site
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JOURNAL
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AUTHORS
TITLE
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AUTHORS
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VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
BX640450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
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Best Local Similarity
                                                                                                                                                                                               TITLE
  JOURNAL
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                                                               Rarkhill, J., Sebaihia, M., Preston, A., Murphy, L.D., Thomson, N., Harris, D.E., Holden, M.T.G., Churcher, C.R., Bentley, S.D., Mungall, K.L., Cerdeno-Tarraga, A.M., Temple, L., James, K., Harris, B., Quail, M.A., Achtman, M., Ackin, R., Baker, S., Basham, D., Bason, N., Cherevach, I., Chillingworth, T., Collins, M., Cronin, A., Davis, P., Doggett, J., Feltwell, T., Goble, A., Hamlin, N., Hauser, H., Holroyd, S., Jagels, K., Leather, S., Woule, S., Worberczak, H., Holroyd, S., Jagels, K., Leather, S., Woule, S., Worberczak, H., Holroyd, S., Jagels, K., Leather, S., Stevens, K., Simmonds, M., Saunders, D., Seeger, K., Sharp, S., Simmonds, M., Seders, M., Saunders, D., Seeger, K., Sharp, S., Simmonds, M., Skelton, J., Squares, S., Stevens, K., Unwin, L., Whitehead, S., Barrell, B.G. and Maskell, D.J.
Comparative analysis of the genome sequences of Bordetella pertussis, Bordetella parapertussis and Bordetella bronchiseptica Nat. Genet. DOI:10.1038/Ng1227-10.1038/Ng1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete genome.

Bordetella bronchiseptica RB50

Bordetella bronchiseptica RB50

Bordetella bronchiseptica RB50

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella bronchiseptica strain
Submitted (06-AUG-2003) Submitted on behalf of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX640450.1 GI:33577349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BX640450 BX470250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCGGTGGACGGGAACGTCCGGAGGGTCCTCTCCCGCCTCTTCGCCCGGGAAAGC 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGTCTCGGGCCTTACACCGCGGCGGCGGTGGCCTCCATCGCCTTCGGGGAGCGGGTGGC 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- CCTGGCCCGAAGCGTGGAGGAGCTTCCCCCGAGCTTCGCCGAGCTTCGGGGGCCTTCC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTCTGGCAGGGGGGGGCTACCGACCGGCGGGGGGGGAACACCTCCACCG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTGGAACGTTTTCCCGATGTGGCCGCCCTGGCGGCGCGCCCAGGAAGATGTCATGCC 139116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTGGAGCGCTTTCCCACCCTGAAGGCCCTGGCCGCGCTTCCCCTGGAAGAGGTCCTTAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCCGAGGTCCTTCTGCAGCAGACCCGGGTGGAGCAGGCCCTCCCCTATTACCGCCGCTT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGCCACGGCCACGATCTGCCCTGGCAGAACACCCGCGACCCCTATCGCATCTGGCT 138996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGCATCGGCCGCTCCACGGCCGCCGATCGCCGCCTTCGCCTACGGCGAGCGCAGCCC 139296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTACTGGGCCGGCCTGGGCTACTACGCGCGCGCGCCAACCTGCACCGCTGCGCGCAGGA 139176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCGGAAATCATGCTGCAGCAGACGCAGGTGGCGACGGTCATTCCGTATTACCAGCGCTT 139056
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                               Submission
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4571. .4621,4637. .4702,4724. .4789,4835. .4900))
/gene="ureJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /locus_tag="BPP3857"
/note="7 probable transmembrane helices predicted for
BPP3857 by TMHMM2.0 at aa 7-29, 44-66, 73-95, 100-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.8%;
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Pred. No. 1e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete genome; segment
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  the Pathogen
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MGAILGT1|EALQLAA|PAHDEALRPAVRAFLDEALREMPADRR RASWMCHDAEFSRALARQGWLGLTLPVEYGGAGRSNFARFVLSEELLAVGAFYSAHWI ADRQTAFLILREGS PAQRAFYLDER|IRGEAFFALGMSEPDTGSDLASVRTRATFVADG WILUNGRKIWTTWAHRSHYMCALVRTSGAPEDHRGLSQMIFDLALPGIEIRPIRDIAG DAHFCEVLFDNVLLPHDALVGEEGSGWRQVWAELALERSGERRYSSNVLLDGWLAHL RRDAAPGRAQVCLAGRLARALAVLSSGNELAVGSGREQADASLAAVLVKDLGTEFEQA VPELIGQALHASPQRADVLARRILAYLITLINPTFSLRGGTRHILRGIIARELGLR" COMDLEMEN (1579...1884)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /locus tag="BB4252"
/note="P800237 G-protein coupled
complement(1888 2244)
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/locus_tag="BB4251"
/note="PS00372 PTS EIIA domains phosphorylation
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/locus_tag="BB4251"
/note="ortholog of Bordetella pertussis (BX470248) BP0421"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /locus_tag="BB4253"
2418. .3395
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Jomplements."

Jocus tag="BB4252"

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/translation="mwtgqyivhiaspahhwrravelrqlkqllvlsetlnfhraaer
Lhmaqpplstaikkleqelgvqlferlpaglqptpaaevvlryaratlfyadbiqraa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /locus_tag="BB4252"
complement(1)??
                                                                                                           /product="LysR-family transcriptional
/protein_id="CAE34617.1"
/db_xref="GI:33577352"
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/product="probable acyl-CoA dehydrogenase"
/protein_id="CAE34616.1"
/db_xref="GI:33577351"
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/protein_id="CAE34615.1"
/db_xref="GI:33577350"
                                                                                                                                                                                                                                                                                   codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                             locus_tag="BB4253"
note="ortholog of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (1120. .2292)

/locus_tag="BB4252"

/note="ortholog of Bordetella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DE Acyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptors
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                                                                                                                                                                                                                       regulator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dehydrogenase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dehydrogenase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            signature
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                                                                                                                                                                                                                                                                                                                                                                                                           BP0419"
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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_
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                                                                                                                                                                                                                                               /locus tag="BB4255"
/note="HMMPfam hit to PF00378, DE Enoyl-CoA hydratase/isomerase family, score 3.9e-50"
/note="tage" 15222. 6454}
                                                                                                                                 complement (5222. .6454)
/locus tag="BB4256"
/note="ortholog of Bordetella pertussis (BX470248) BP0416"
                                                                                                                                                                                                                                                                                                                                                                                   /translation="MTDFLRHERHGGVLLLIMDRERTRNALSDADAVEALVQACARIG ADLSVRAVVLTGSHGVFSSGGNLKTLSDTVGAGLGEPVHSRAVERSGIGRIFLALYNL EVPTLAAVNERGEAGRIERLARYNL REVPTLAAVNERGEAGREAGEDACKMCHERTARGASFAESFVKLGLIFGDGGAWLLPRIVG MSRACELAFTGRSIDAARARELGIVSEVFDADALLPALALAQBIAQHSGHALRLTKR LAREGQHTRLDTLELSAGFQALAHHTQEHAGALDAHLSRKRG"
                                                                                                                                                                                                       /locus_tag="BB4256"
complement/cocc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /locus_tag="BB4255"
complement(4444. .5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Signal peptide predicted for BB4254 by Signalp 2.0 MMM (Signal peptide probabilty 1.000) with cleavage site probability 0.873 between residues 24 and 25; signal-peptide site" complement (3418. .4236)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="HMMPfam hit to PF03401, family, UPF0065, score 4.4e-85" complement (4444...5229)
'translation="MSGPLEGVRILDVTTVLMGPYATQILGDLGADVIKVEPPAGDNV
                          'product="conserved hypothetical protein"
'protein_id="CAE34620.1"
'db_xref="GI:33577355"
                                                                                                         codon_start=1
transI_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="probable enoyl-CoA hydratase"
/protein_id="CAE34619.1"
/db_xref="GI:33577354"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /BC_number="4.2.1.17"
/note="ortholog of Bordetella pertussis (BX470248) BP0417"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MHSRTLALALLS VAALAQGGSARAASDYPAHPVKIIVSLPPGGG
ADTTARFLSKHLAERFKRPFVVENRPGGNSFIAQQAVATAPPGVGTTLFVASNSPMTTN
AAVFKNLPYDAVKDFAPVAFIARFPMALVVPANSPYRSVADLVAAARAADGQLNFASG
TATYQVVLBLFHEQNGIKATHVPYKGTSAALADVAGGVVQYSVADVSAALPLIRGGKL
RPLAVTSTRRIKGLPDVPTMQESGNKGFEAYAMTAAFFPAKVDPAIVARVSDAVQALV
RPLAVTSTRRIKGLPDVPTMQESGNKGFEAYAMTAAFFPAKVDPAIVARVSDAVQALV
RSQBGKAFMEQLGGBEFVGGPDTLAAFQRDELASMRRIAKLANIQQE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative exported protein"
/protein_id="CAB34618.1"
/db_xref="GI:33577353"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /locus_tags"BB4253"
/note="HMMPfam hit to PF03466,
domain, score 3.1e-43"
complement(3406. .4377)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QBGASGKQGMLKVGFVGSSIYSLMPQLLSAFRKDYPRVDLVIEESTTVDLLRRLDAHT
LDVALVAF PVLEBSTARITLLGADHLMLAVPAGGSRVAGORDDVALDELADEFFIGYSRT
HVPGMHALINVAFQQYGVVPHIAQEALQVQTILSLVESGLGLAIVPKVACRQAGSGVR
LVNVPQLAETKVGIALAVHPDNATPTTANFVDMACRLMQTEPAAGQAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (4306. .4377)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /locus_tag="BB4254"
complement/2401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               signature
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/locus tag="BB4253"
/note="HMMPfam hit to PF00126,
/note="HMMPfam bit to PF00126,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus_tag="BB4254"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="ortholog of Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="PS00044 Bacterial regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 locus_tag="BB4255"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     locus
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18_tag="BB4254"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tag="BB4253"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .5229)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DE Uncharacterized protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DE LysR substrate binding
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REFERENCE
AUTHORS
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ORGANISM
                                                                                                                         VERSION
KEYWORDS
                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                   RESULT 10
SCO939116
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                                                                                                                                                                                                                                                                                                                                           220141 CATCATGGACGGCAACGTCAAGCGGGGTGTTCACGCGCACTTCGGCATCGAGGGC 220195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 TOTGGAGOGOTTTCCCACCCTGAAGGCCCTGGCCGCGGCTTCCCTGGAAGAGGTCCTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250;
                                                                                                                                                             SCU939116 293050 bp DNA linear BCT 11-FEB. Streptomyces coelicolor A3(2) complete genome; segment 13/29. AL039116 AL035636 AL049573 AL049628 AL049630 AL049645 AL049661 AL049707 AL049763 AL049819 AL049841 AL079345 AL133236 AL133255 AL645882
                                                         Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
    Bentley, S.D.,
                                          Streptomycineae;
                                                                                                                                            AL939116.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTACTGGGCCGGCCTGGGCTACTACGCGCGGGCCGGCAACCTGCACCGCTGCGCGCAGGA 220020
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGTCTCGGGCCTTACACCGCGGCGGCGGCGGTCGCCTTCCATCGCCTTCGGGGAGCGGGTGGC 380
                                                                                                                                                                                                                                                                                                                                                                                   GGCGGTGGACGGGAACGTCCGGAGGGTCCTCTCCCGCCTCTTCGCCCGGGAAAGC 435
                                                                                                                                                                                                                                                                                                                                                                                                                           CGGCATCGGCCGCCACGGCCGCCGCCATCGCCCTTCGCCTACGGCGAGCGCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- CCTGGCCCGAAGCGTGGAGGAGCTTCCCCCGAGCTTCGCCGAGCTTCGGGGGCTTCC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTCTGGCAGGGGGCTACTACCGGCGGGGGGGAACACCTCCACCG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGCCACGGCCACGATCTGCCCTGGCAGAACACCCGCGACCCCTATCGCATCTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCGGAAATCATGCTGCAGCAGACGCAGGTGGCGACGGTCATTCCGTATTACCAGCGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCCGAGGTCCTTCTGCAGCAGACCCGGGTGGAGCAGGCCCTCCCCTATTACCGCCGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative membrane protein"
/protein id="CAB34621.1"
/protein id="CAB34621.1"
/db_xref="GI:33577356"
/translation="MDYLVSLAQQPAAWAALATLIAMEVVLGIDNLIFISILTNKLPP
/CHQTKARRIGIGMALILRLALLGTVAFIVQLTQPVFELFGHGFSWRDVILVAGGLFLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WKATKEIHHHVDPNPGDDMFGGKAATLGFAAAVAQILMLDLVFSIDSIITAVGMTEHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGIGBGRHADMGGIFLHANRSKRSIALDLKNPAGREALLKVAATCDVLVYNVRPQAMA
RLGLSYAEVAQANPSILYVGWYGYDQKEPYAARAAYDDLIQGAVGIPSLSVEAGSDIF
RYABSAMVDRIVGISAANAVTAGLYHRARTGOGOAIDVPMFETMAHLILGDHMYGOTE
EPPLGPPGYPRILNADRRPYATRNGHICVLLYADKHWKAFFELLIGQPGRDAADPRFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (6650.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGAATAAARQLPEGTDHD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGTRTQHIHAIYRLVSDAIASRTTEEWLAAFEAADIPAMPVHTMASLLRDPHLEAIGF
FGMVDHPSEGAVRMMAVPSRWSGTPPQPRGHAPRLGEHSVDVLKEAGYDDEAIAALVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(6650. .7405)

Locus tag="BB4257"

Locus tag="critics of Bordetella pertussis"

Locus tag="critics of Bordetella pertussis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="HMMPfam hit to PF02515,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
transI_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'locus_tag="BB4257"
                                                                                                                                            GI:24413781
  Chater, K.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.8%;
                                        Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 135; DB 1
Pred. No. 1e-09;
0; Mismatches 1
Cerdeno-Tarraga, A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .7405)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .6250)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 346287;
                                    Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE CAIB/BAIF family, score
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                                                                                                                                                                                                                                           BCT 11-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155
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Challis, G.L.,

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JOURNAL
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TITLE
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Complete genome sequence of the model actinomycete Streptomyces
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Nature 417 (6885), 141-147 (2002)
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/note="SCE39.33c, possible precorrin-6X reductase from Rhodococcus sp. (248 aa) fasta scores; opt:
255 aa; similar to many e.g. SW:COBK_RHOSO precorrin-6X
reductase from Rhodococcus sp. (248 aa) fasta scores; opt:
873, 2-score: 978.5, E(): 0, (55.1% identity in 247 aa
overlap) and SW:COBK_MYCTU precorrin-6X reductase from
Mycobacterium tuberculosis (244 aa) fasta scores; opt:
690, 2-score: 775.5, E(): 0, (50.4% identity in 244 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="SCE39.32, possible precorrin-8X methylmutase, len: 218 aa; sinilar to many e.g. SW.COBH PSEDE Precorrin-8X methylmutase from Pseudomonas denitrīficans (210 aa) fasta scores; opt: 868, z-score; 1000.1, E(): 0, (64.2% identity in 204 aa overlap) and SW:COBH MYCTU precorrin-8X methylmutase from Mycobacterium tuberculosis (208 aa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="Sptrembl:Q9x8f5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fasta scores; opt: 852, z-score: 982.0, E(): 0, (64.1%
identity in 206 as overlap)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (745. .1512)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="SC03282"
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/note="SCE15:01, partial CDS, conserved hypothetical protein, len: >436aa; similar to C-terminal region of TR:CAA22732 (EMBL:AL035161) another conserved hypothetical protein from Streptomyces coelicolor (860 aa) fasta scores; opt: 922, z-score: 1011.5, E(): 0, (39.5% identity in 425 aa overlap).

SCE39.34, unknown, len: >307aa; similar to TR:E1370406 (EMBL:AL035161) conserved hypothetical protein from Streptomyces coelicolor (860 aa) fasta scores; opt: 254, z-score: 277.0, E(): 4e-08, (29.2% identity in 277 aa overlap) TR:O86875 (EMBL:122894) hypothetical protein from Streptomyces lividans (547 aa) fasta scores; opt: 226, z-score: 249.7, E(): 1.3e-06, (33.0% identity in 197 aa
LTABLE BALLORS WINDERSON OF THE PROPERTIES OF THE PROPERTY OF 
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GLTRGNGDEGBAARRRLEHILASTTRFLQELCDTAVTHWAPSRHDDAVLLLARTRALF

DEHVLDWTLPADASVGGTARRLVDRQLASWGLDEAATTTGLVZELVTMAIRXGKGFV
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EGPRPPRTEVLLDRGPFTLDGERELLRRHRIDVLVTKDSGGAATAPKLTAAREAGLPV
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complement(3855. .9173)
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Query Match
Best Local &
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CCTTCGGGGAGCGGTGGACGGGAACGTCCGGAGGGTCCTCTCCCGCCTCT 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTCCTCGCTACCCGGAAAACGCCCCCTCCCTCCCTGGCGG----GGAGAAGG
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//gene="SC03286"
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//mote="SCE15.03, putative secreted protein, len: 677 aa;
//mote="SCE15.03, putative secreted protein from Escherichia coli (553 aa) fasta scores; opt: 542, z-score:
S01.2, E(): 1.3e-20, (27.0% identity in 504 aa overlap).
Contains possible N-terminal region signal peptide
sequence also contains a highly hidrophilic central part
//codon start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGRTILRLGAHRFAVNTQPLDLTILVPDGDGLAFALTGTDYRSPVTDPDFAATRAHWDRT
LPSESPGVYRAEHLAARLLRQHGASALAAADDLFALVREAAQEAYDEGYERGVHDHDA
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LDDHYTAEAQTLTHGAEANLLKLAELRGTLTPEQADRWAEVTTAHVRARTLGGPDDDP
LTRAVAALGLLADRVAAVESAITRAAADPRHLLANPHARHAAGGTER"
COMMI-TAMPART (1930)
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FLRTEEQLGVQRENQAREVAVAAKNRERVIAVENERIEKDRMLEAIGRERETELTRIA
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Pred. No. 2.6e-09;
0; Mismatches 293;
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CGTACGGCCAGCGGCACGCCGTGCTGGACACCAACGTCCGCCGGGTCCTCGCCCGGCGCGG 89920

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Submitted (05-DEC-2000) Takakazu Kaneko, K
Institute, The First Laboratory for Plant
1532-3, Kisarazu, Chiba 292-0812, Japan
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Mesorhizobium loti DNA, complete genome, section
AP003012 BA000012
AP003012.2 GI:14026948
                                                                                                                                                                                                                                                                                                                                                           (E-mail:kaneko@kazusa.or.jp, Trizobase/, URL:http://www.kazusa.or.jp/rhizobase/, Tel:81-438-52-3936/ex.2338/ rax:81-438-52-3934) On May 11, 2001 this sequence version replaced g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti DNA Res. 7 (6), 331-338 (2000)
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Mesorhizobium loti
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1. .346547
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                                                                                                                                                                                                                                                                                              complement (5644. .6240)
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complement(5644...6240)
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2122. .27
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ADDAALVKASFAALPAPARSDFGINVLPGDHETLVVEASFPGDPEAADFFVAGERDYM
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db_xref="GI:14027001"
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ANTFVIEDSVHGVAGARAAGMRVIGFTGASHSYPGHADALTBAGAETVIRRWAELKSV
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/gene="mll7517"
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/gene="ml17519"
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/gene="mll7517"
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QYAQYVGGDFREDRDLMDAQIVLGFEGRAYHVRDFYASQVLSMILGGGMSSRLFQEVR
EKRGLCYSVYAFHMGFSDTGIFGVHAATGQSDIAELVPVIIDELQKAGENILQEELDR
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codon_start=1
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transl_table=11
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RESULT 12
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Streptomyces antibioticus
gene, complete cds.
AF121797
2 (bases 1 to 1106)
Bralley, P. and Jones, G.H.
Transcriptional analysis
                                                                                                                                                                   Jones, G.H., Paget, M.S., Chamberlin, L. and Sigma-E is required for the production of actinomycin in Streptomyces antibloticus Mol. Microbiol. 23 (1), 169-178 (1997)
                                                                                                                                                                                                                                                                                                                                         Streptomyces antibioticus
Bacteria; Actinobacteria; Actinobacteridae; Actinobacteria; Streptomyces
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Pred. No. 4.5e-09;
D; Mismatches 233;
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18 A/G-specific
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Bralley, P. and Jones, G.H.
Direct Submission
Submitted (19-JAN-1999) Biology,
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Biochim. Biophys. Acta 1517
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/product="A/G-specific adenine glycosylase"
/product="A/G-specific adenine glycosylase"
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/protein_id="AAD21076.1"
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RLHGAAVWAITERHGGDVVGTTAQLIALDGIGEYTAARWAASMELGALVCTAKWETCRVC
PIAGQCAWRLAGKPEHDGPPRRGQTYAGTDRQVRGKLLAVLREAHAPVPQEALDQVWQ
EPVQPPRALDGLVPPDGLVEPLPGGTYRLPLT"
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Location/Qualifiers
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/function="DNA mismatch
/note="MutY"
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183. .1106
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/clone="pJSE1101"
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/mol_type="genomic DNA"
/strain="IMRU 3720"
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Nierman, W.C., Feldblyum, T.V., Paulsen, I.T., Nelson, K.E., Eisen, J.,
Nierman, W.C., Feldblyum, T.V., Paulsen, I.T., Nelson, K.E., Potocka, I.,
Heidelberg, J.F., Alley, M.R.K., Ohta, N., Maddock, J.R., Potocka, I.,
Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B.,
Laub, M.T., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L.,
Laub, M.T., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L.,
Haft, D.H., Kolonay, J.F., Smit, J., Craven, M., Khouri, H., Shetty, J.,
Berry, K., Utterback, T., Tran, K., Wolf, A., Vamathevan, J.,
Ermoleva, M., White, O., Salzberg, S.L., Shapiro, L., Venter, J.C. and
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Nierman, W.C., Feldblyum, T.V., Laub, M.T., Paulsen, T.T., Nelson, K.E. Eisen, J., Heidelberg, J.F., Alley, M.R., Ohta, N., Maddock, J.R., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Haft, D.H., Kolonay, J.F., Smit, J., Craven, M.B., Khouri, H., Shetty, J., Berry, K., Utterback, T., Tran, K., Wolf, A., Vamathevan, J. Ermolaeva, M., White, O., Salzberg, S.L., Venter, J.C., Shapiro, L. and Prace, C.
                                                                                                                                                                                                                   Submitted (31-JAN-2001) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers
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Caulobacter crescentus CB15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete genome sequence of Caulobacter crescentus Proc. Natl. Acad. Sci. U.S.A. 98 (7), 4136-4141 (2001)
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/gene="CC0365"
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codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                        complement (2475.
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                                                                                                          ACCAAGAAGGCCGACCGGCGCACGGCACGGCGTGGCCTATGTGCTGACGCGCG 10885
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TITLE larimer, F. M., Chain, P., Hauser, L., Lamerdin, J., Malfatti, S., I Lard, M., Chain, P., Hauser, L., Lamerdin, J., Malfatti, S., I Land, M.L., Pelletier, D.A., Beatty, T.J., Lang, A.S., Tabita, F.R. Gibson, J.L., Hanson, T.E., Torres y Torres, J., Peres, C., Harrison, F.H., Gibson, J. and Harwood, C.S. Rhodopseudomonas palustris CGA009 Rhodopseudomonas palustris CGA009 Bacteria; Proteobacteria; Alphaproteobacteria; Bradyrhizobiaceae; Rhodopseudomonas. Complete genome sequence of the metabolically versatile complete genomes. BX572607 BX571963 BX572607.1 GI:39651254 BX572607 3450: Rhodopseudomonas palustris BX572607 BX571963 345012 bp tris CGA009 complete genome; Rhizobiales; BCT 18-DEC-2003 segment 15/16. Do, L.,

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JOURNAL
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome consortium, the DOB Joint Genome Institute, Production Genomics Facility, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA, and the Genome Analysis Group, Oak Ridge National Laboratory, 1060 Commerce Park Drive, Oak Ridge, TN 37831, USA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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Larimer, F.W. and Harwood, C.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /txanslation="msargcegepquvtgahdwliaavlldmdgtludterlyleslt
Evlnafglpdaistcesnvglpgbecqallvarygetlplreinrafvekrdarfaqg
Lpvkpgtcelldalddagcpvavvtsssrktadmhltlagirarfatiltrddvvhgk
Papdlyllaanrlgvppahcvavedssvgvasaftagaitlmvpdllqpddatrgkca
Vlpdlmavrslleirgrpaapdaalapr"
                                                                                                                                                                                                                                                                                                                                                                                                                          /locus_tag="RPA4338"
complement(2341. .3021)
/locus_tag="RPA4338"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1671.
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EASLKKLKTDWIDLYQQHDYDFLTFIDETLRALDDLIRAGKVRY YGNSNFPAWRIAEA
EYVARALGTHRYVSCQDEYSLVVRDIEKDLLPAAQEYKLGLLPFFPLASGLLTICKYQR
GTEAPAHTRFAKMPAIRDRYFTDANLDLVDKLKGFAEARGHSLLELAFSWLACRPQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function="Interpro IPR001395 COGs COG0667"
/note="observed by proteomics
Citation: Proteomics from VerBerkmoes et al. (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVIAGATTPEQIEQNVKAVSWKLTAEEMAEVDAITKG"
                                                                                                                 <u>ARQMLLLLDGSFAVVLLHRDPSYMETAGAAAAKLVAAALPRSFNAARGPRPAPRTGRG</u>
                                                                                                                                      KAGVTKRTLYYHFRSKDDLVAAYLEGRDQPNLALFRQWFEETPGELPAKVEGIFRNLA
RAARHPKWKGCGFLRTSAELANLPGHPAIKIGAAHKKKFERWLRETFAEAGITEADEL
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/evidence=not_experimental
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (2341. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
/product="putative phosphoglycolate phosphatase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative oxidoreductase"
/protein_id="CAE29777.1"
/db_xref="GI:39651255"
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function="InterPro IPR005834:IPR006402 COG8 COG0637"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MDIRNLGGSGLRVSVVGLGCNNFGQRTDPETSKKVIHKAIDLGV"
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strain="CGA009"
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locus_tag="RPA4339"
103. .3894
                                                     103. .3894
                                                                                                                                                                                                  translation="MAVRVSVAPKAPPPSPTRDRIVAAAAKLFYSEGIRAVGVDAVAE
                                                                                                                                                                                                                                                                                                                                                                                                     function="InterPro IPR001647 COGs COG1309"
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QAQLNIASGLEQVAERY QVRCIDI DANVTI VEGDTGLI ITDTTLTVQTAKAALDLYYQ
AMSRRAJOFQFCTQLF VEGRAGOVDAGLGKALAKGTVSI IAPUBLI KQPYETRS IDGVEI
EFHLVPESEAPSEMI SYYPQFKVLIMAREDTTHTLHNLYTLRGAAI ROGRLWSKY IGEA
IERYGGKTDVVI AQHHWPVWGRDR VVGYLKKQRDVYKF IHDQSVRLLNHGLTPTE IAB
RLTLPPSLTSEFAARGYYGSVSHNAKAVYQFYLGWYDANPADLNPLPRAEQAKKEIDY
MGGAAAVLARARDDYKAGQYRWVATVASKLVFADPANTEARALGADALEQLGKKEIDY
TWRNYLLGAADELRNGLI KTDSVTSNEDDLKGVSI DLAFDFLAVRLNAKAEGKHIVV
NWTFTDLKETYMNLENSALTHISGKLSDNADVSVTLNRATFDAISLKORGFLGAVLS
GDLWYSGNPLKLRELFGLFEDDFSPNFEVI EPVKAKVE"
                                                                                                                                                                                                                                         /locus____
.8143
                                                                                                                                                                                                                                                                                                                                            /locus_tag="RPA4341"
/note="Signal predicted by SignalP 2.0 HMM (Signal peptideprobabilty 1.000) with cleavage site probability 0.916 atresidue 26"
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complement(3882. .4685)
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complement (3882..4685)
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IVHLLMYAGALIVISAMGLFSTMAFAGLGGAALTATALIYAVAFWWTGHYLWHVKNLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (6782.
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/locus_tag="RPA4341"
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PEDAAYFRQSREARLKTTLEEAAASRDRAVQGFRKSLDPLRLTLKTQAFIGGAAFNYA
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complement(4874
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VGADAGRPFSPFVWRTRMALAHKGLTAETIPWRFTDKAAIAPYGSEKVPVLLDGDKVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="putative lignin beta-ether hydrolase"
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/product="possible crotonase,
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/evidence=not_experimental
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transl_table=11
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Best Local Similarity
Matches 377; Conserv
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      ACGTCCGGAGGGTCCTCTCCCGCCTCTTCGCCCGGGAAAGC-----CCCAAGGAGAAGG 448
                                                                 ACACAGCCGCCGCGATCGCCGATTGCGTTCAGCCGCCGGACGATGCCGGTCGACGGCA 172679
                                                                                                                                                                                            ATGGAGGCCGCTTTCCCGACACCGAGGAGGGGGCTGCGGGCCCGGCCCGGCCGT 172739
                                                                                                                                                                                                                                                                                                                 TCGGCTACTACTCACGCGCCCCCCAATCTGCACGCCTGCGCGGTGGCGGTGACGCGCCAGC 172799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCACCCTGAAGGCCCTGGCCGCGCTTCCCTGGAAGAGGTCCTTAGGGTCTGGCAGGGGG
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/transl_table=11
/product="possible excinuclease ABC subunit B"
/product="possible excinuclease ABC subunit B'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     order(7232. .7300,7313. .7381,7400. .7459,7517. .7585,
7604. .7663,7706. .7759,7778. .7846,7889. .7957,7994.
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ALVALAFYRFPFIVFLMAVALWFLSMDLVPWITGTPHGDFETGKRVSIGFGAVMVIAA
VIVHLRQRSGDPAFMLYLFGYMTFWGGITATSMGTNLDKALYCAMNVVFLGIAVVLGR
RVFAVFGALGIAIYLGDLAEKLFRDSLLFPFALSLIGIAIIALGLFLHRRLPAIEAWC
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/function="InterPro
IPR001410:IPR001650:IPR001687:IPR001943:IPR004807 COGS
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9650. .11238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /locus_tag="RPA4342"
/note="9 probable tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----AAGGACCCTTACCGCGTCCTGGTCTCCGAGGTCCTTC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 124.4; DB 1;
Pred. No. 2.7e-08;
0; Mismatches 316;
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JOURNAL
MEDLINE
PUBMED
REFERENCE
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 11034)
Ng,W.V., Kennedy,S.P., Mahairas,G.G., Berquist,B., Pan,M.,
Shukla,H.D., Lasky,S.R., Baliga,N., Thorsson,V., Sbrogna,J.,
Shukla,H.D., Lasky,S.R., Baliga,N., Thorsson,V., Sbrogna,J.,
Swartzell,S., Weir,D., Hall,J., Dahl,T.A., Welti,R., Goo,Y.A.,
Leithauser,B., Keller,K., Cruz,R., Danson,M.J., Hough,D.W.,
Maddocks,D.G., Jablonski,P.E., Krebs,M.P., Angevrine,C.M., Dale,H.,
Isenbarger,T.A., Peck,R.F., Pohlschrod,M., Spudich,J.L.,
Jung,K.-H., Alam,M., Freitas,T., Hou,S., Daniels,C.J., Dennis,P.P.,
Omer,A.D., Ebhardt,H., Lowe,T.M., Liang,P., Riley,M., Hood,L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11016950
2 (bases
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Shukla,H.D., Lasky,S.R., Baliga,N., Torsson,V., Sbrogna,J.,
Swartzell,S., Weir,D., Hall,J., Dahl,T.A., Welti,R., Goo,Y.A.,
Leithauser,B., Keller,K., Cruz,R., Danson,M.J., Hough,D.W.,
Maddocks,D.G., Jablonski,P.E., Krebs,M.P., Angevine,C.M., Dale,H.,
Isenbarger,T.A., Peck,R.F., Pohlschrod,M., Spudich,J.L.,
Jung,K.-H., Alam,M., Freitas,T., Hou,S., Daniels,C.J., Dennis,P.P.,
Omer,A.D., Ebhardt,H., Lowe,T.M., Liang,P., Riley,M., Hood,L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Halobacterium sp. NRC-1
Halobacterium sp. NRC-1
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
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Halobacterium sp. NRC-1 section
AE005065 AE004437
AE005065.1 GI:10581001
                                                                                                                                                                                                                                                                                                                                                  Submitted (14-JUL-2000) Institute for Systems Roosevelt Way NE, Seattle, WA 98105, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of Halobacterium species NRC-1
Proc. Natl. Acad. Sci. U.S.A. 97 (22), 12176-12181 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                DasSarma,S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCTTTTCGCCCTCGCCCAGGGCCTCCTCCCCGAGGGCGTGGACCCGGGGGTGTGGAACC
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                                                                 /gene="VNG1510C"
complement/~
                                                                                                                              /db_xref="taxon:64091"
complement(70. .1719)
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
   complement(70. .1719)
/gene="VNG1510C"
/note="conserved hypothetical protein"
                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="NRC-1"
                                                                                                                                                                                                                                                   organism="Halobacterium"
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BCT 12-FEB-2001

Biology,

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Search completed: March
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APPLICANT: MARC J. RUBENFIELD AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
SEQ ID NO 6832
LENGTH: 963
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APPLICANT: Marc J.
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Patent No. 6551795
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ORGANISM: Pseudomonas aeruginosa
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US-08-690-473-1
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SUMMARIES

Issued_Patents_NA:*

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US-09-543-853-010-4
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Sequence 6886, Application US/09252991A

Patent NO. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
ENGTH: 1401
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; ORGANISM: Pseudomonas
US-09-252-991A-6886
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Pred. No. 2.2e-16;
0; Mismatches 231;
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107195.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6739
LENGTH: 1413
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 4788
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6783, Application US/09252991A
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                                                                                    TGTGTCCGCTGAGCAACGGCTGCGTGGCCTACGCGAACC
                                                                                                                 CCTGCCCCTAGGGGCCTTCTGCCGGGGGAAGGAGGCCC
                                                                                                                                                                                                                                                CCCTCGCCCAGGGCCTCCTCCCCGAGGGCGTGGACCCCGGGGGTGTGG----
                                                                                                                                                                                                                                                                               TGAAGCGCGTGCTCGCCCGCTGCTATGCTGTCAGCGGCTGGCCGGGGAAAAAAAGAGGTGG
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Pred. No. 6e-14;
0; Mismatches 245;
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; Patent No. 6551795
; GENERAL INFORMATION:
APPLICANT: MARC J. RUBENIELE ACID AND AMINO AUTILE OF INVENTION: NUCLEIC ACID AND AMINO AUTILE OF INVENTION: ABRUGINOSA FOR DIAGNOSTIFILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6783
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6783
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                                                                                                                                                                                             RESULT 6
                                                                  Sequence 1, Application US/08813574
Patent No. 6013473
GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fei
TITLE OF INVENTION: Human Muty
NUMBER OF SEQUENCES: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
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                                                                                                                                                                                                                                                                                                                                                                                                                               GCGGCGGCGGTGGCCTCCATCGCCTTCGGGGAGCGGGTGGCGGCGGTGGACGGGAACGTC
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                                                                                                                                                                                                                                                     AGGGCGCTGTGGGAAGCCCGCAACGCTTCACCCCG 515
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                                                                                                                                                                                                                                                                                                                                                                                               GCTGGAGCCATCGCCAGCCTGTCGATGGGCCTGCGCGCACCGATCCTCGACGGCAACGTC
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
NUCLEIC ACID AND DIAGNOSTICS AND THERAPEUTICS
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Pred. No. 7.5e-13;
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

Diskette

STATE: PA COUNTRY: US

USA

PA

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US-08-813-574-1
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/813,574
FILING DATE:
CLASSIFICATION DATA:
CLASSIFICATION DATA:
APPLICATION UMBER: 60/013,132
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG50002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Sin
Matches 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 54.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1858 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
1038
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                                                                                                            GGAGCTCGGGGCCACGGTCTGCCTGCCGAAACGGCCCGGTTGCGGGGCCTGCCCCTAGG 578
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GAGCCTGTGCCGGG
                                                                                                                                                                                             GCCTCCTCCCCGAGGCGTGGACCCG------GGGGTGTGGAAACCAGGCCCTCAT
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                                     GCCTTCTGCCGGG
                                                                     GGAGCTAGGGGCCACAGTGTGTACCCCACAGCGCCCACTGTGCAGCCAGTGCCCTGTGGA 1037
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                                     592
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188 617

797 350 737 300

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RESULT

7

SOFTWARE: 1

PatentIn Ver. 2.1

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> 977 518 917 468 857

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FEQUENCE 38, Application US/09650855

PATENT NO. 6365355

GENERAL INFORMATION:
APPLICANT: MCCUTHEN-MALONEY, SANDRA
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
TITLE OF INVENTION: MUTATIONS, DNA SEQUENCE VARIATIONS, DNA
TITLE OF INVENTION: MUTATIONS, DNA
TITLE OF INVENTION: MUTATIONS, DNA
TITLE OF INVENTION: MUTATIONS, DNA
TITLE OF INVENTION MUTATIONS, DNA
TITLE OF INVENTION NUMBER: US/09/650,855

CURRENT APPLICATION NUMBER: 60/192,764
PRIOR FILING DATE: 2000-03-28

NUMBER OF SEQ ID NOS: 106
SOPTWARE: DATE: 2000-03-28

NUMBER OF SEQ ID NOS: 106
SOPTWARE: DATE: 2000-03-28
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; SEQ ID NO 38
; LENGTH: 2293
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-651-656-38
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US-09-650-855-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: MCCUTHEN-MALONEY, SANDRA
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
APPLICANT: LOUIS DITECTION AND QUANTITATION OF SINGLE NUCLEOTIDE
TITLE OF INVENTION: DOLLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTI-
TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
FILE REFERENCE: IL-10689
FULE REFERENCE: IL-10689
CURRENT APPLICATION NUMBER: US/09/651,656
CURRENT PILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: 60/192,764
PRIOR APPLICATION NUMBER: 60/192,764
PRIOR PILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity 54.1%;
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Pred. No. 7.2e-09;
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; LENGTH: 2293 ; TYPE: DNA ; ORGANISM: Escherichia US-09-650-855-38

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Length 2293;

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RESULT 9
US-09-103-840A-2
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Matches 210; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: FILEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/99/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09103840A Patent No. 6294328
                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: WHITE, OWEN R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                   LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                         FEATURE:
                                     4022631
                                                                                                      Match 8.9%;
Local Similarity 50.2%;
es 345; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACAAACTCAGGTTGCGACCGTTATCCCCTATTTTGAACGCTTTATGGCGCGCTTCCCCGA
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                                                        CTCCTCGCCTGGTACCGGGAAAACGCCCCCCCCCCCCCTGGCGGGGG----GAGAAGGAC
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                                       CCTTACCGCGTCCTGGTCTCCGAGGTCCTTCTGCAGCAGACCCGGGTGGAGCAGGCCCTC 138
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Pred. No. 7.2e-09;
0; Mismatches 163;
                                                                                                           <u>.</u>
                                                                                                           Score 86.6; DB 3;
Pred. No. 1.8e-08;
0; Mismatches 309;
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                                                                                                                                             Length 4403765
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DIA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VEY: 2
SOFTWARE: PATENTIN VEY: 2
SEQ ID NO 1
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US-09-103-840A-1
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Query Match
Best Local S
Matches 345
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Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                     LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4022871 CACGAGTGCGCCACCGTCATCGCCCGCGACCACAATGACGTGGTGCCCGACGATATCGAG
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                                8.9%;
Score 86.6; DB 3;
Pred. No. 1.8e-08;
0; Mismatches 309;
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                                                                       Length 4411529
          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IN MYCOBACTERIUM
   33; Gaps
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Length 9909; Indels

15;

Gaps

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RESULT 11
US-08-961-527-12/c
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                 SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Charles Kuni
TITLE OF INVENTION: SC:
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4031207
                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                   20850
                                                                                                                                                                                                                                                                     Rockville
: Maryland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACGGCCGCCCGACGCCGGTGCCCATCGGTGCCGCGGGCGACCACGCCGACGTCTTGGCG 4031029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACGAGTGCGCCACCGTCATCGCCCGCGACCACAATGACGTGGTGCCCGACGATATCGAG 4030849
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9410 Key West Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                     Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                   391
                                                                                             US/08/961,527
                                                                                                                                                                                         3.50 inch, 1.4Mb storage
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US-09-107-532A-3654
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 9909 base pairs
TYDEP.
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                                                                                                                                                                                                                                                                                                       Sequence 3654, Application US/09107532A
PATENT NO. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear US-08-961-527-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.4%;
Best Local Similarity 52.2%;
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Brookes, A. Ar REGISTRATION NUMBER:
                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5508
                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5448 AACTTGCCTGAGCCAGCTGTAGATGGTAATGTCATGCGGGTCTTGGCGCGTCTGTTTG 5391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 TACCGCGTCCTGGTCTCCGAGGTCCTTCTGCAGCAGACCCCGGGTGGAGCAGGCCCTCCCC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 CTCCTCGCCTGGTACCGGGAAAACGCCCGCCCCCTCCCCTGGCGGGGGGGAGAAGGACCCT 81
                                                                                                                                                           ZIP: 02354
                                                                                                                                                                                             STATE: Massachusetts
                                                                                                                                                                                                                 CITY: Waltham
                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGAGCGGGTGGCGGGGGGGGGGGGGGGGGGGGCTCTTCG 424
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Pred. No. 8.5e-08;
0; Mismatches 185;
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and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FABCIUM FOR DIAGNOSTICS AND THERAPEUT

THERAPEUTICS

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3654:
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APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1212 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...1212
SEQUENCE DESCRIPTION: SEQ ID NO: 3654:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO
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                                                                                                                                  GGCGTGGACCCCGGGGTGTGGAACCAGGCCCTCATGGAGCTCGGGGCCACGGTCTGCCTG
                                                                                                                                                                            GACATCGCAAAAGCTTCTAGCAGGAAAATCTTTGATGAAGCGATGCGGAAAATCATTGAT 579
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    CCAACTTCTCCAAAGTGTGAGACTTGTCCGATCCAAGCCTTTTG
                                            CCGAAACGGCCCCGTTGCGGGGCCTGCCCCCTAGGGGGCCTTCTG 587
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Pred. No. 0.00029;
0; Mismatches 279;
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Sequence 1710, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FO)
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
NUMBER OF SEQ ID NOS: 6812
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US-09-134-000C-1710
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SEQ ID NO 1710
LENGTH: 1188
TYPE: DNA
ORGANISM: Enterococcus faecalis
                                                                                                                                                Sequence 23, Applicat Patent No. 6232106 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.4%;
Best Local Similarity 48.8%;
Matches 211; Conservative
                                                Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
                                                                                APPLICANT: Susan E. Jensen
APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequer
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE,
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                                                                                                                                                                                   Application US/09385028
                                                                                   DNA Sequence Encoding
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Pred. No. 0.0005;
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REGISTRATION NUMBER: 1418
REFERENCE/DOCKET NUMBER: 1418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-6666
TELEFAX: (202) 39305350
TELEFAX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1227 base pairs
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Best Local Similarity
Matches 345; Conserv
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APPLICATION NUMBER: US 00
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. Douglas Price
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/385,028
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
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CAGGTCGCCAAGGCCCGGGACGAACTCGACGGCTATCTGCGGGAGCTGGTCGAGGAGCGG
                                                                CGCCGGGAGTTCATCGAGGACCGCAGCGCGGTCCTCATCGACCGCGGCTACACCCCGGAG
                                                                                                CCCCTAGGGGCCTTCTGCCGGGGAAGGAGGCCCCCGGGCGCCTACCCCGCGCCCAGGAAG
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Pred. No. 0.00055;
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RESULT 15
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APPLICANT: Kwamena A Aidoo
APPLICANT: Abhish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6514735
TITLE OF INVENTION: Acid Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESSPONDENCE ADDRESS:
CORRESSPONDENCE ADDRESS:
                                                                                                           Query Match
Best Local Similarity 44.4
.---- 345; Conservative
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GENERAL INFORMATION:
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ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION NUMBER: US/09/726,614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. DOUGLAS Price
REGISTRATION UNMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 39305350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA
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CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                    DNA (genomic)
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                                                                                                                                     Score 62.2; DB 4;
pred. No. 0.00055;
0; Mismatches 423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version
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871 808	811 748	751 688	691 628	631 568	571 508	511 448	451 388	393 328	337 268	277 208	217 148
GGGAGGACCCCTGGAAGAGGCCCCTACCCAAGCTCATGGAGAAGGTGCTCCGC 924	CACGCCCTCACCCGAAGGCTTCGCGTGGAGGTGCGGGGGGGG	GAGCTTCCCGGGCGGGAGGCGCCTTCGGGGGTGAGGTCTAGGCCCCTAGGCGAGGTGCGC 810	CTGGAAAGGCTTCAGGGGCCTCTACGGCGTCCCCCTCTTTCCCCCCTGAG 750	CGCCGGGCGAAGGAGGAGCGCCTCGTCCTCCTCCTCCGGGCGGAAGGGGGTGCAC 690	CCCCTAGGGGCCTTCTGCCGGGGAAGGAGGACCCCCGGGGCCTACCCCGCGCCCAGGAAG 630	GCCTCATGGAGCTCGGGGCCACGGTCTGCCTGCCGAAACGGCCCCGTTGCGGGGCCTGC 570	CTTTTCGCCCTCGCCCAGGGCCTCCCCCGAGGGCGTGGACCCGGGGGTGTGGAACCAG 510	GAACGTCCGGAGGGTCCTCTCCCCCCCTCTTCGCCCCGGGAAAGCCCCAAGGAGAAGGAG 450	ACCGCGGCGGCGGTGGCCTCCATCGCCTTCGGGGAGCGGGTGGCCGCGGTGGACGG 392	GTGGAGGAGCTTCCCCGGAGCTTCGCCGAGCTTCCGGGGCCTTAC 336	GTCTGGCAGGGGGGGGCTACTACCGGCGGGGGGGGAACACCTCCCACCGCCTGGCCCGAAGC 276

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Search completed: October 8, 2004, 05:13:15
Job time: 114 secs

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Match Length
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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Copyright (c) 1993 - 2003 Compu
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US-09-925-301-1326

US-10-156-761-12241

US-09-738-626-6433

US-09-864-866-43

US-09-864-866-43

US-09-912-020-296

US-09-912-020-296

US-10-128-714-3128

US-10-128-714-3128

US-10-128-714-3128

US-09-840-743-1

US-09-840-743-8

US-09-840-743-8

US-09-840-743-8

US-09-840-743-8

US-09-840-743-8

US-09-840-743-8

US-09-840-743-8

US-10-302-840A6
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(without alignments)
718.508 million cell updates/sec
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Sequence 2, Appli
Sequence 1324, Ap
Sequence 1224, A
Sequence 1324, A
Sequence 6433, Appl
Sequence 12127, A
Sequence 12127, Ap
Sequence 328, Ap
Sequence 3128, Ap
Sequence 8128, Ap
Sequence 8128, Ap
Sequence 11, Appl
Sequence 2, Appli
Sequence 8, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 14029, A
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ALIGNMENTS

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RESULT 1

US-09-938-901-2

Sequence 2, Application US/09938901

Publication No. US20030008291A1

GENERAL INFORMATION:
APPLICANT: Kuramitsu Seiki,
APPLICANT: YOKOYama Shigeyuki
TITLE OF INVENTION: GENE ENCODING DNA REPAIR ENZYME
FILE REFERENCE: PH-1261-US
CURRENT APPLICATION NUMBER: US/09/938,901

CURRENT FILING DATE: 2001-08-24
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SEQ ID NO 2
LENGTH: 325
TYPE: PRT
                                                                                                                                                                                                                                                        Query Match 100.0%; Score 1700; DB 11; Best Local Similarity 100.0%; Pred. No. 2.6e-152; Matches 325; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP2001-47762
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 17
                                      121
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181 LPKRPRCGACPLGAFCRGKEAPGRYPAPRKRRAKEERLVALVLLGRKGVHLERLEGRFQG
                                                                                                          AFGERVAAVDGNVRRVLSRLFARESPKEKELFALAQGLLPEGVDPGVWNQALMELGATVC 180
                                      AFGERVAAVDGNVRRVLSRLFARESPKEKELFALAQGLLPEGVDPGVWNQALMELGATVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1326, Application US/09925301 Patent No. US20020052308A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: SITE
LOCATION: (447)
OTHER INFORMATION: Xaa equals
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LOCATION: (438)
OTHER INFORMATION: Xaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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Local Similarity 36.6%;
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                                                                                                                                                                                                                                                                                                                                                                               104 VTAFRGSLLSWYDQEKRDLPWRRRAEDEMDLDRRAYAVWVSEVMLQQTQVATVINYYTGW 163
 279 RVEVRGALWEGE 290
                                                                                                    343 CAPNTGQCHLCLPPSEPWDQTLGVVNFPRKASRKPPREESSATCVLEQPGALGAQILLVQ
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                                                                                                                                                                                                                                                                                                              164 MQKWPTLQDLASASLEEVNQLWAGLGYYSRGRRLQEGARKVVEELGGHMPRTAETLQQLL
                                                                                                                                                                                                                                                                                                                                            53 LERFPTLKALAAASLEEVLRVWQGAGYYRRAEHLHRLARS-VEEL---PPSFAEL--RGL
                                                                                                                                                                                                                                                                                                                                                                                                               1 VEAWRKALLAWYRENARPLPWRG-----EKDPYRVLVSEVLLQQTRVEQALPYYRRF
                                                                                                                                                                                           KLMEKVLRKALPLLAHAGVVPLPDA 325
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                                                                                                                                                                       PARPGDFNQAAMELGATVCTPQRPLCSQCPVESLCRARQRVEQEQLLASGSLSGSPDVEE
                                                                                                                                                                                                                                         PGVGRYTAGAIASIAFGQATGVVDGNVARVLCRVRAIGADPSSTLVSQQLWGLAQQLV-D
                                                                                                                                                                                                                                                                        PGLGPYTAAAVASIAFGERVAAVDGNVRRVLSRLFA----RESPKEKELFALAQGLLPE 161
                                  RPNSGLLAGLWEFPSVTWEPSEQLQRKALLQELQRXAGPLPATHXRHLGEVVHTFSHIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 486.5; DB 9
Pred. No. 1.9e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9;
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                                                                                                                                                                                           US-09-738-626-6433 Application US/09738626 Sequence 6433, Application US/09738626 publication No. US20020197605A1 GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Streptomyces avermitilis US-10-156-761-12241
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US-10-156-761-12241
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SEQ ID NO 12241
LENGTH: 313
TYPE: PRT
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Best Local :
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APPLICANT:
APPLICANT:
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APPLICANT:
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
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                     APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
       REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
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97; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVASIAFGERVAAVDGNVRRVLSRLF-----ARESPKEKELFALAQGLLPEGVDPGV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLAKEAPGEAVRAWGRLGYPRRALRLHGAAVAITERHNGDVPTEHAQLLALPGIGEYTAA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EALHAQVIAWFDEHARDLPWRRPDAGPWGVMVSEFMLQQTPVNRVLPVYEQWLARWPRPA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EAWRKALLAWYRENARPLPW-RGEKDPYRVLVSEVLLQQTRVEQALPYYRRFLERFPTLK 60
                                                                                                        HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
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HORIKAWA, HIROSHI
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                                                                                           TATEISHI, NAOKO
                                                                                                                                                          ANDO, SEIKO
                                                                                                                                                                          MIZOGUCHI, HIROSHI
                                                                      SENOH, AKIHIRO
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                                                                                                                                                                                                                                                                                                                                     265
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Pred. No. 2.3e
32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 15;
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GENERAL INFORMATION:

APPLICANT: LLOYd, R. Stephen

APPLICANT: McCullough, Amanda K.

APPLICANT: McCullough, Amanda K.

APPLICANT: Nguyen, Khoa

FITLE OF INVENTION: DNA REPAIR POLYPEPTIDES AND METHODS OF USE

FILE REFERENCE: 265.00170101

CURRENT APPLICATION NUMBER: US/09/864,866

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/206,279

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

NUMBER OF SEQ ID NOS: 49

SOFTWARE: Patentin version 3.0
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN Ver. 3.0
SEQ ID NO 6433
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US-09-864-866-43
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; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6433
                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 43
LENGTH: 268
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Best Local Similarity
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CURRENT FILING DATE: 2000-12-18
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44
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                                                                                                                                                                                                                        Similarity
                                                                                                                   PYRVLVSEVLLQQT---RVEQALPYYRRFLERFPTLKALAAASLEEVLRVWQGAGYYR-R
                                                                                 PFELLVATVLSAQTTDVRVNAATP---ALFARFPDAHAMAAATEPELQELVRSTGFYRNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIMDVLRNATAPVPLSAIDVVWPDDAQRSRALFSLIEDGLAEQNEA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VHLERLEGREQ--GLYGVPLFPPEELPGREAAFGVRSRPLGEVRHA 272
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32.4%;
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                                                                                                                                                                                         Score 199; DB 10;
Pred. No. 1.2e-10;
31; Mismatches 95;
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                                                                                                                                                                                                                                              Length 268;
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                                                                                                                                                                                                                  RESULT 7
US-09-738-626-3828
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                                                  GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROS
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12127
LENGTH: 310
                                                                                                                                                             Sequence 3828, Application US/09738626 Publication No. US20020197605A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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PRIOR APPLICATION NUMBER: JP 2
PRIOR AFFECTION NUMBER: JP 2
PRIOR AFFETTION NUMBER: JP 2
PRIOR AF
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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION UMBER: US/10/156,761
CURRENT FILLING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
APPLICANT:
                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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Local Similarity 25.8%;
Local Similarity 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 NPEEVEEILRPTGFFRAKTKSVIGLSKALVEEFGGEVPGRLEDLVKLPGVGRKTAFVVLG 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                       RRICHARKPACGACPIAPLCPAYGEGETDPEKAKKLLKYE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RENARPLPWRGE----KDPYRVLVSEVLLQQT---RVEQALPYYRRFLERFPTLKALAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSYAAGETDPERARALLAYELKPGREELLELLRAGR 255
                                                                                                                                                                                                                                                                                                                          ---GFPGQRLNPPQAYLD---AGGIPAPPLG
                                                                                                                                                                                                                                                                                                                                                                               RFQGLYGVPLFPPEELPGREAAFGVRSRPLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAFGRPGITVDTHFQRLVRRWQWTDEKDPDKIEAAVGALFPK----SEWTMLSHHVIFHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLEEVLRVWQGAGYYR-RAEHLHRLARSV-----EELPPSFAELRGLPGLGPYTAAAVAS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RELAEVYPYAHPELDFENSFQLILATVLSAQTTDLRVNQTTP---ALFAKYPTPEDLAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASAILRLSQELVGRHDGEVPARLEDLVALPGVGRKTAFVVLGNAFGQPGITVDTHFGRLA 160
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HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                              MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HORIKAWA, JUN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 184.5; DB 1
; Pred. No. 3.5e-09;
44; Mismatches 110
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Gaps

121

176

279 236 237

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APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 3828
LENGTH: 260
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-3828
                                                                                                                                 APPLICANT: Froelich, Jamle M.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
FILE REFERENCE: ELITRA.001DV1
CURRENT APPLICATION NUMBER: US/09/912,020
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 485
us-09-912-020-296
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                                                                     SEQ ID NO 296
LENGTH: 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zyskind, Judith
APPLICANT: Ohlsen, Kari L.
APPLICANT: Trawick, John
APPLICANT: Forsyth, R. Allyn
                                                                                                                SOFTWARE: FastSEQ for Windows Version
                   ORGANISM: E. Coli
                                                 TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 KATSLIGLGEALISLHDGQVPGTLEQLVELPGVGRKTANVVLGNAFGVPGITVDTHFGRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 NPLELTVATILSAQCTDVRVNQVTP---ALFKRYPTATDYANADRTELEEFIRPTGFYRN 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 DPYRVLVSEVLLQQ----TRVEQALPYYRRFLERFPTLKALAAASLEEVLRVWQGAGYYR-
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US-10-128-714-3128
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SEQ ID NO 3118
LENGTH: 281
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
FILE REFERENCE: 10182-018-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 8603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengi
                                                                                                                                                                                                                                                                                     Local
                                                                             157 MAYLCMSAAWGKDEGIGVDVHVHRI-TNLWGWHKTKTPEETRMALESWLPR----DKWHE
                                                                                                                      113 TAAAVASIAFG-ERVAAVDGNVRRVLSRLFARESPKEKELFALA-QGLLPEGVDPGVW--
                                      169 -NQALMELGATVCLPKRPRCGACPLGA--FCRGK 199
                                                                                                                                                                 97 LENILAVSPEKLNELIRTVGFHNNKTKYIKAAAEILRDQYNSDIPSTAEELMKLPGVGPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117
                                                                                                                                                                                                        59 LKALAAASLEEVLRVWQGAGYYRRAEHLHRLARSV-----EELPPSFAELRGLPGLGPY 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 KVDCHHW---LILHGRYTCIARKPRCGSCIIEDLCEYKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 GVDPGVWNQALMELGATVCLPKRPRCGACPLGAFCRGKE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 LGPYTAAAVASIAFGERVAAVDGNVRRVLSRL-FAR----ESPKEKELFALAQGLLPE-- 161
                                                                                                                                                                                                                                                                   44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 VANTPAAMLELGVEGVKTYIKTIGLYNSKAENIIKTCRILLEQHNGEVPEDRAALEALPG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 ---TLKALAAASLEEVLRVWQGAGYYR-RAEHLHRLARSV-----EELPPSEAELRGLPG 108
                                                                                                                                                                                                                                                          h 7.5%; Score 128; DB 15; Similarity 28.6%; Pred. No. 0.00066; 44; Conservative 26; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 KAKRLEILTRLRENNPHPTTELNFSSPFELLIAVLLSAQATDVSVNKAT-----AKLYP 56
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INKLLVGLGQTVCLPVGRRCGECDLAGTKLCKSE 245
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29.2%; Pred. No. 1.1e-05;
33. Mismatches 88;
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APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Methods of Use FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT APPLICATION NUMBER: US/60/287,714
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-23
PRIOR TILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
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US-10-128-714-8128
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 8128
SEQ ID NO 11
LENGTH: 1332
                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/09840743 Publication No. US20030135890A1
                                                                                    APPLICANT: Fischer, Robert L.
APPLICANT: Choi, Yeonhee
APPLICANT: Hannon, Mike
APPLICANT: Hannon, Mike
APPLICANT: Okamuro, Jack Kishiro
APPLICANT: Tetarinova, Tattiana Valerievna
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids That Control Plant Development
FILE REFERENCE: 023070-099910US
CURRENT APPLICATION NUMBER: US/9/840,743
CURRENT APPLICATION NUMBER: US 09/553,690
PRIOR APPLICATION NUMBER: US 09/553,690
PRIOR FILING DATE: 2000-04-21
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APPLICANT:
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PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
                                             NUMBER OF SEQ ID NOS: 119
SOFTWARE: PATERTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 INKLLVGLGQTVCLPVGRRCGECDLAGTKLCKSE 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 LKALAAASLEEVLRVWQGAGYYRRAEHLHRLARSV-----EELPPSFAELRGLPGLGPY 112
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Similarity 28.6%; Pred. No. 0.0013;
44; Conservative 26; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAYLCMSAAWGKDEGIGVDVHVHRI-TNLWGWHKTKTPEETRMALESWLPR----DKWHE 391
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Tishkoff, Daniel
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Best Local Similarity
Whiches 51; Conserve
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; OTHER INFORMATION: DEMETER (DMT)
US-09-840-743-2
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SEQ ID NO 2
LENGTH: 1729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tatarinova, Tatiana Valerievna
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids That Control Plant Development
FILE REFERENCE: 023070-099910US
CURRENT APPLICATION NUMBER: US/09/840,743
CURRENT FILING DATE: 2001-04-23
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APPLICANT: Choi, Yeonhee
APPLICANT: Hannon, Mike
APPLICANT: Okamuro, Jack Kisl
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TYPE: PRT
ORGANISM: Arabidopsis thaliana
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1339 SIQKFLWPRLCKLDQRTLYELHYQLITFGKVFCTKSRPNCNACPMRGECRHFASAYASAR 1398
                                                                                                                                                            1219 EAIRRASISEISEAIKERGMNNMLAVRIKDELERIVKDHGGIDLEWLRESPPDKAKDYLL 1278
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                                     162 GVDPGVW-------NQALMELGATVCLPKRPRCGACPLGAFCR---GKEAPGR 204
                                                                                                                    105 GLPGLGPYTAAAVASIAFGERVAAVDGNVRRVLSRLF---ARESPKEKELFALAQGLLPE 161
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                                                                                                                                                                                                    60 KALAAASLEEVLRVWQGAGY-----YRRAEHLHRLARS------VEELPPSFAE--LR 104
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59; Conserv
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                                                                               SIRGLGLKSVECVRLLTLHNLAFPVDTNVGRIAVRMGWVPLQPLPESLQLHLLELYPVLE
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22.3%;
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22.8%; Pred. No. 0.16;
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US-10-302-840A-6
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/10302840A Publication No. US20030134794A1 GENERAL INFORMATION:
                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 6
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Matches
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                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/302,840A CURRENT FILING DATE: 2003-01-24 PRIOR APPLICATION NUMBER: 60/332,015 PRIOR FILING DATE: 2001-11-20 NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 1413
                                                                                                                                                                                                                                                                                     APPLICANT: Ong, Edgar O.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING SERINE PROTEASE CVSP17,
TITLE OF INVENTION: POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: 24745-1622
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Madison, APPLICANT: Ong, Ed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tatainova, Tatiana Valerievna
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids That Control Plant Dev
FILE REFERENCE: 023070-099910US
CURRENT APPLICATION NUMBER: US/09/840,743
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 09/553,690
PRIOR FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 119
            NAME/KEY: DOMAIN
LOCATION: (104)...(332)
OTHER INFORMATION: CVSP17 protease
                                                                                       LENGTH: 635
TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fischer, Robert L.
APPLICANT: Choi, Yeonhee
APPLICANT: Hannon, Mike
APPLICANT: Okamuro, Jack Kis
                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: DMT2 (1DMT2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 FALAQGLLPEGVDPGVW------NQALMEL-----GATVCLPKRPRCGACPLGAFCR 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             946 PPDKAKEYLLSFNGLGLKSVECVRLLTLHHLAFPVDTNVGRIAVRLGWVPLQPLPESLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         886 KAIRAADVKEVAETIKSRGMNHKLAERIQYLTLNMKIMQGFLDRLVNDHGSIDLEWLRDV 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 6.5%; Score 110;
Similarity 23.3%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPSFAE--LRGLPGLGPYTAAAVASIAFGERVAAVDGNVRRVLSRLF---ARESPKEKEL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LALP----APEERSLTSAT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14029
LENGTH: 549
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
CURRENT FILING DATE: 2002-05-29
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340 AVLARAVAEELASIGVPVLLGVRPVEGRVPLLLGLRSES-----
                                                                                                                                                                                                                                172 VPQVLRILADFSGNPVFLETADGRLLYAAGAGPADTDPLQVWEGL----RGQH-----
                                                                                                                                                                                                                                                                                                            112 ALVETARTAGLPLVQLHREVPFVTVTEEVHTEIVNGHYALLQRAEEVHRRCTEALLGGGG
                                                                                                                                                                                       93 VEELPPSFAELRGLPGLGPYTAAAVASIAF---GERVAAVD-----GNVRRVL----
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                                                                                                                                                     -KDAPPAGTTIVDVPGGGPGAGSVRARLVLLPVGNPVAPVHRIAAERAAGSLAVVLMQAR 279
                                                                                                                                                                                                                                                                       -PYYRRFLERF---PTLKALAAASL-----EEVLRVWQGAGYYRRAEHLHRLARS
                                    -----NQALMELGATVCLPKRPRCGACPLGAFCRGKEAPGRYPAPRKRRAKEERLVAL 221
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HORIKAWA, HIROSHI
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Pred. No. 0.14;
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Search o	DЪ	Qy	рь	Qy	Db	ОУ
Search completed: September 15, 2003, 14:02:48 Job time : 69 secs	492 TYLAHAG 498	314LAHAG 318	441 RPWYDARRLDIDLLLWRLR-DDPDLAAFVDRAIGPLRDHDNRSKPPLLPTLQ 491	264 RPLGEVRHALTHRRLRVEVRGALWEGEGEDDWKRPLPKLMEKVLRKALPL 313	391 LRAGVERAGMORPGAOPPVVVVGVAGGWAAASAGLRHAAQTATAAQGLSD 440	GVPLFPPEELPGR

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Result
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Perfect score:
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length: 2000000000
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Gapop 10.0 , Gapext 0.5
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compus
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ABP56413
ABB54155
ABP79054
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621.520 Million cell updates/sec
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24 24 24 21 19 23 23 22

Protein involved i

Escherichia

coli

Human cancer assoc Human mismatch rep

N. gonorrhoeae ami Lactococcus lactis

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DNA repair ransformant equence of	; 2003- SDB; AE	$\overline{}$	FEB-2001;	FEB-2001;	SEP-2002	JP2002247985	hermus the	Thermus thermophilus; TRCF; biochemistry; m	Thermus the	MAR-2003	ABP56413;	T 1 413 ABP56413 st		159.5	161.5	16	164	4.		172.5	η. ω	ω μ	20	274.5	4.4			3 68 3 0 0 3 0 0	437	44.	442.5	59.	0 #	n .	
r enzyme gene, t, preparation a DNA, and pre	078924/08 8222143.	RIKAGAKU KENKYUSHO	; 2001JP-0047762	; 2001JP-0047762	•	5-A.	thermophilus	rmophilu emistry;	thermophilus	(first		standard;		9.4													19.6								27.4 27.4
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e, a protein, a on of DNA repai prevention of e								pair enzyme; r biology; r	air enzyme		•	325 AA.	ALIGNMENTS	ABP38380 AAG17150	AAU29544	ABP25506	AAG81939	AAW23155	ABB54387	ABP65491	ABB48015	ABP25507	AAB96207	AAW48738	AAW11703	ABP07225	AAU41327	ABP27944	AAW25524	AAY86014	ABP65978	ABU01657 ABP39839	AAY37104	AAW60244	AAY09118 ABP27945
in, a recombinant vector, a repair enzyme, repairing the error of error synthesis of a DNA sequence								e; enzyme; MutY; RecJ; RecF; research.	MutY protein SEQ ID NO:2.				NTS	Stapnylococcus epi Arabidopsis thalia	Novel human secret	Streptococcus poly	s. epidermidis ope	Human endonuclease	Helicobacter pylor Lactococcus lactis	Bifidobacterium lo	Listeria monocytog	Streptococcus Intens	Putative P. abyssi	ORF10 glycosylase.	ORF10 thermally st	Human ORFX protein	Propionibacterium	Streptococcus poly	Aniho acid sequenc Staphylococcus aur	S. pneumoniae deri	Bifidobacterium lo S. pneumoniae muty	S. pneumoniae type Staphylococcus epi	Protein involved i	mino acid of the	eumonia tococcu

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RESULT 2
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Best Local S
Matches 325
The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The
                                 Claim
                                                                                                  Bolotine
                                                                                                                  (INRG ) INRA INST NAT RECH AGRONOMIQUE
                                                                                                                                      11-APR-2000;
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                                                                                                                                                                                                                                   Biosynthesis;
                                                                                                                                                                           12-OCT-2001.
                                                                                                                                                                                                                Lactococcus lactis
                                                                                                                                                                                                                                                  Lactococcus lactis protein muty.
                                                                                                                                                                                                                                                                         16-MAY-2002
                                                                                                                                                                                                                                                                                                            ABB54155 standard;
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MutY, Rec
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                                                   nucleotide sequence useful in tis and related species -
                                                                               2002-043418/06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to ABZ22146 encode the Thermus thermophilus DNA repair enzymes cJ, RecF, and TRCF given in ABP56413 to ABP56416. The enzymes sed as research reagents for biochemistry and molecular biology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALAAASLEEVLRVWQGAGYYRRAEHLHRLARSVEELPPSFAELRGLPGLGPYTAAAVASI
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                                                                                                Sorokine A,
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                              2504pp;
                                                                                               Renault P,
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                              French.
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RESULT 3
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Best Local :
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    The present invention Also disclosed are the
                                                            New protein from Neisseria gonorrheae, medicament for treating or preventing |
                                     Disclosure; Page 528; 815pp; English.
                                                                                                          N-PSDB;
                                                                                                                                              Fontana
                                                                                                                                                                      (CHIR-) CHIRON SPA
                                                                                                                                                                                              12-FEB-2001; 2001GB-0003424
                                                                                                                                                                                                                     12-FEB-2002; 2002WO-IB02069
                                                                                                                                                                                                                                                10-OCT-2002.
                                                                                                                                                                                                                                                                        WO200279243-A2
                                                                                                                                                                                                                                                                                               Neisseria gonorrhoeae.
                                                                                                                                                                                                                                                                                                                       Antibacterial; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                 N. gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                            07-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                           ABP79054 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid sequence is useful in the detection and/or amplification nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent W0200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                     ABP79054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                              MR,
                                                                                                        ABZ40024.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIASISFGLAEPAIDGNLMRVTSRLFELDCDISKSSSRKIF---DGYLRKLISKKRPGDF
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Pred. No. 3.1e-38;
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encoding the proteins a
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Matches 128
                                                                                                                                                                                                                                               Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antistrhritic; antiviral; antiinflammatory; antitstyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; antipsoriatic; artispassass; organ rejection; allergic reaction; graft versus host disease; organ rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoe infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention.
                                                                                                                                                                                                                                                                                                                                                                                            Human
                  Rosen
                                              (HUMA-) HUMAN GENOME SCI INC
                                                                          12-MAR-1999;
                                                                                                     08-MAR-2000;
                                                                                                                                   21-SEP-2000
                                                                                                                                                                WO200055350-A1
                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                          haemostatic;
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                CA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATVCKRTKPLCRQCPMADICEAKKQNRTAELPRKKTALEVQTLPLYWLIVRNRDGAILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATVCLPKRPRCGACPLGAFCRGKEAPGRYPAPRKRRAKEER---LVALVLLGRKG-VHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FNRRETILDGNVKRVLCRVFAQDGNPQDKKFENSLWTLAESLMPSENADMPTYTQGLMDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGERVAAVDGNVRRVLSRLFARE-SPKEKE----LFALAQGLLP-EGVDPGVWNQALMEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QDEVLSLWAGLGYYGRARNLHKAAQQIVGQFGGTFPSERKDLETLCGVGRSTAAAISAFA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEEVLRVWQGAGYYRRAEHLHRLARSV-----EELPPSFAELRGLPGLGPYTAAAVASIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIRWQKQHGRHHLPWQ-VKNPYCVWLSEIMLQQTQVAAVLDYYPRFLEKFPTVQTLAAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLAWYRENAR-PLPWRGEKDPYRVLVSEVLLQQTRVEQALPYYRRELERFPTLKALAAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKRTAKGIWGGLYCVPCF -- ESLNGLSDFAAKLSLIMADMDEQTALIHRLIHRLLMIT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ER--LEGRFQGLYGVPLFPPEELPGRE---AAFGVRSRPLGE---VRHALTHRRLRVEVR
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                  Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                           thrombolytic; cardiovascular disorder; disease; drug screening.
                                                                                                       2000WO-US05882
                                                                                                                                                                                                                                                                                                                                                                                          associated protein sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₹
                                                                          99US-0124270
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38.1%;
                                                                                                                                                                                                                         drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 491; DB 24;
Pred. No. 3.4e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Å
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104;
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                                                                                                                                                                                                                                         infection;
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RESULT 5
AAW31912
ID AAW3
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AC AAW3
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AAW31912 st; AAW31912; 27-MAR-1998

(first entry)

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB4240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         include: cytostatic; proliferative; vulnerary; immunomodulator;
antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in AAB43398 to AAB44239. The proteins can have activities based on tissues and cells the genes are expressed in. Example of activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acids comprising sequences useful for treating or diagnosing e.g. cancer - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 1976–1978; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-587533/55
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                                                                                                                                                                                                                                    GVDPGVWNQALMELGATVCLPKRPRCGACPLGAFCRGKE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEAWRKALLAWYRENARPLPWRG-----EKDPYRVLVSEVLLQQTRVEQALPYYRRF
TYQVYGLALEGQ
                                                                                                                                            CAPNTGQCHLCLPPSEPWDQTLGVVNFPRKASRKPPREESSATCVLEQPGALGAQILLVQ
                                                                                                                                                                                                                                                                                                           PGLGPYTAAAVASIAFGERVAAVDGNVRRVLSRLFA-----RESPKEKELFALAQGLLPE 161
                                                                                                                                                                                                                                                                                                                                                               MQKWPTLQDLASASLEEVNQLWAGLGYYSRGRRLQEGARKVVEELGGHMPRTAETLQQLL
                                                                                                                                                                                                                                                                                                                                                                                      LERFPTLKALAAASLEEVLRVWQGAGYYRRAEHLHRLARS-VEEL---PPSFAEL--RGL
                                                                                                                                                                                                                                                                                                                                                                                                                                    VTAFRGSLLSWYDQEKRDLPWRRRAEDEMDLDRRAYAVWVSEVMLQQTQVATVINYYTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to AAC78448 encode the human
                                   RVEVRGALWEGE
                                                                                                          R-LEGREQGLYGVP--LEPPEELPGREAAF----
                                                                                                                                                                                                                   PARPGDFNQAAMELGATVCTPQRPLCSQCPVESLCRARQRVEQEQLLASGSLSGSPDVEE
                                                                        RPNSGLLAGLWEFPSVTWEPSEQLQRKALLQELQRXAGPLPATHXRHLGEVVHTFSHIKL
                                                                                                                                                                                   -AP-----
                                                                                                                                                                                                                                                                                          PGVGRYTAGAIASIAFGQATGVVDGNVARVLCRVRAIGADPSSTLVSQQLWGLAQQLV-D
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 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 486.5; DB Pred. No. 1.4e-37
                                                                                                                                                                             -GRYPAPRKRRAK---EERLVALVL----LGRKGVHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer associated proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107;
                                                                                             -GVRSRPLGEVRHALTHRRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83;
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on the
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Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                This protein comprises human Mutty, which is homologous to the Escherichia coli Mutty protein involved in the pathway that corrects A/G and A/C mismatches as well as adenines paired with 7,8-dihydro-8-oxo-deoxygunaine in mutated DNA. Its amino acid sequence was deduced from a human cerebellum cDNA clone (see AAT89194). Muty polypeptides can be expressed in transformed host cells. The polypeptides can be expressed in concoding them, can be used e.g. to repair oxidative damage to DNA, to prevent mutations from oxidative lesions, to treat genetic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding human MutY protein - useful for detecting and treating mismatches in DNA especially in non-polyposis colon cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MutY; hMYH gene; mismatch repair; non-polyposis colon cancer;
xeroderma pigmentosum; gene therapy; diagnosis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human mismatch repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                           related to a mutated hMYH gene, e.g. xeroderma pigmentosum and neoplasia, and to diagnose an abnormal transformation or a susceptibility to abnormal transformation of cells, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ( HUMA - )
                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1997-470811/43
                                                                                                                                                                                                                                                                                                                                                                                                               non-polyposis colon cancer.
                                                                                                                                         162
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                                                                                                                                                                                                                                     79
                                                                                                                                                                                                                                                                                           1 VEAWRKALLAWYRENARPLPWRG------EKDPYRVLVSEVLLQQTRVEQALPYYRRF
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SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 39-40; 59pp; English
                                                                                                             VTAFRGSLLSWYDQEKRDLPWRRRAEDEMDLDRRAYAVWVSEVMLQQTQVATVINYYTGW
                                R-LEGREQGLYGVP--LEPPEELPGREAAF------GVRSRPLGEVRHALTHRRL
                                                           CAPNTGQCHLCLPPSEPWDQTLGVVNFPRKASRKPPREESSATCVLEQPGALGAQILLVQ
                                                                                                                                                                    PGVGRYTAGAIASIAFGQATGVVDGNVARVLCRVRAIGADPSSTLVSQQLWGLAQQLV-D
                                                                                                                                                                                             PGLGPYTAAAVASIAFGERVAAVDGNVRRVLSRLFA----RESPKEKELFALAQGLLPE
                                                                                                                                                                                                                       MQKWPTLQDLASASLEEVNQLWAGLGYYSRGRRLQEGARKVVEELGGHMPRTAETLQQLL
     RPNSGLLAGLWEFPSVTWEPSEQLQRKALLQELQRWAGPLPATHLRHLGEVVHTFSHIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pigmentosum
                                                                                                                                                                                                                                                                                                                                                                                      535 AA;
                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-US03239
                                                                                                                                                                                                                                                                                                                                             28.5%; Score 484.5; DB 18; 36.6%; Pred. No. 2.5e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein MutY
                                                                                                                                                                                                                                                                                                                                 46;
                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                      -GRYPAPRKRRAK---EERLVALVL----LGRKGVHLE
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AAW60243
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents human MYH (hMYH). The MYH polypeptide can be used for diagnosing cancer, where the decreasing levels of the polypeptide are measured in a sample from a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Pages 20-21; 23pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polypeptide - useful for, e.g. diagnosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-210407/19
N-PSDB; AAV35701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; MYH; hMYH; diagnosis; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of human MYH (hMYH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW60243 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                 139
                                                                               201
                                                                                                                                                                                                                                 53 LERFPTLKALAAASLEEVLRVWQGAGYYRRAEHLHRLARS-VEEL---PPSFAEL--RGL 106
                                                                                                                                                                                                                                                                      79
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                                                                                                                                                                                                                                                                    VTAFRGSLLSWYDQEKRDLPWRRRAEDEMDLDRRAYAVWVSEVMLQQTQVATVINYYTGW
                                                                                                                                                                                                                                                                                     VEAWRKALLAWYRENARPLPWRG------EKDPYRVLVSEVLLQQTRVEQALPYYRRF 52
                                                                                                       PARPGDENQAAMELGATVCTPQRPLCSQCPVESLCRARQRVEQEQLLASGSLSGSPDVEE
                                                                                                                        PGLGPYTAAAVASIAFGERVAAVDGNVRRVLSRLFA-----RESPKEKELFALAQGLLPE
RPNSGLLAGLWEFPSVTWEPSEQLQRKALLQELQRWAGPLPATHLRHLGEVVHTFSHIKL
                         ---EGRFQGLYGVP--LFPPEELPGREAAF------GVRSRPLGEVRHALTHRRL
                                                                                                                                                             PGVGRYTAGAIASIAFGQATGVVDGNVARVLCRVRAIGADPSSTLVSQQLWGLAQQLV-D
                                                                                                                                                                                                                   MQKWPTLQDLASASLEEVNQLWAGLGYYSRGRRLQEGARKVVEELGGHMPRTAETLQQLL
                                                   CAPNTGQCHLCLPPSEPWDQTLGVVNFPRKASRKPPREQSSATCVLEQPGALGAQILLVQ
                                                                                -APG-----
                                                                                                                                                                                                                                                                                                                                                                               535 AA;
                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0013132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97JP-0099540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "nucleotides encoding this residue
                                                                                                                                                                                                                                                                                                                                       28.5%; Score 484.5; DB 19; 34.9%; Pred No. 2.5e-37;
                                                                                                                                                                                                                                                                                                                            49; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     535 AA
                                                                               ----RYPAPRKRRAKEERLVALVLLGRKGVHLERL----
                                                                                                                                                                                                                                                                                                                               Indels
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83;

Gaps

11;

138

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200

257 161 198

317

377

234

not given"

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                                                                                             The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for ralsing specific antibodies, identification of L. monocytogenes and related organisms, and for blosynthesis and biodegradation, especially biosynthesis of Vitamin 112. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Buchrleser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux Dussurget O, Checouani F, Nedjari H, Glaser P, Kunst F, Cossar Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N, Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chakrawa, Bayuun Perez-Diaz J, Bayuun Bayuun Perez-in E, De Pablos
                                                     specification,
                                                                                     monocytogenes and related organisms
                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                related
                                                                                                                                                                                                                                                                                                                                                                                                            Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-010914/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB49175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB49175 standard; Protein;
                                   ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279
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                                                                                                                                                                                                                                                                                                                                                              6;
                                                                                                                                                                                                                                                                                                                                                                                              polypeptides
                                                                                                                                                                                                                                                                                                                                                              SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVEVRGALWEGE
                                                 sequence data for this patent did not form tion, but was obtained in electronic format
   365
                                                                                                                                                                                                                                                                                                                                                              IJ
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                                                                                                                                                                                                                                                                                                                                                             No 1880; 192pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wil F, Nedjari H,
Kreft J, Kuhn
Garrido
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                                                                                                                                                                                                                                                                                                                                                             French.
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                                                 part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                for treatment
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Cossart
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Query Match Best Local S Matches 104

Similarity

28.1%;

Conservative

70;

Score 478; DB 23; Pred. No. 6.3e-37; 0; Mismatches 126

Length 365; Indels

38;

Gaps

10;

Sequence

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RESULT 8
AAY35003
ID AAY3
                   C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AN234584-X35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising
especially where the vector directs the expression epitope of {\tt C.} pneumoniae.
                                                                                                                                                                                                                                                                                                                                   Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-357842/30
                                                                                                                                                                                                                                                                                                                                                                                                                                Griffais
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21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Respiratory sinusitis; p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY35003;
                                                                                                                                                                                                             frames in the complete genome
                                                                                                                                                                                                                                           AAY34584-Y35879 represent the
                                                                                                                                                                                                                                                                                       Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEST ) GENSET
                                                                                                                                                                                                                                                                                     906-907; Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s; purulent of neutralising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AILSIAYNQAEPAVDGNVMRVIARVLEIGEDIMKASTRKIFEEVLYQLIDKKNPAAFNQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLVWKMDIRVAKLQSAIPNENWYFATEEEMKRLAFPVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVASIAFGERVAAVDGNVRRVLSRLFA----RESPKEKELFALAQGLLPEGVDPGVWNQA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFVNADEADILKAWEGLGYYSRVRNLQTAMKQVMADFSGEVPTDLTTILSLKGVGPYTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LMEIGALVCTPTKPMCMLCPLQPFCEAHKNGVETNYPVKIKKVKMKTKELLSIIVISEDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease;
purulent o
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97FR-0014673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pneumonia; bronchitis; heart disease; sarcoidosis; otitis media; erythema nodosum; pharyngitis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intermediate metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                  1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375
                                                                                                                                                                                                             proteins encoded by all the open readings (see AAX91990) of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ą
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RESULT 9
AND69755
ID AND6
XX AND6
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Best Local Similarity
             Sequences
                                                       Disclosure; Page 98-99; 128pp; English.
                                                                                                                              Recombinant chimeric protein, useful for detecting and quantifying mutations, e.g. in disease diagnosis, comprises mutation-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA damage; human xeroderma plgmentosum complementation group; XPF; XPA; XPC; XPE; ERCC4; human MutS homologue 2; hMSH2; kutS; Nuc; MutY; Fpg; Fapy-DNA glycosylase; urgcil DNA glycosylase; ung; TDG; xthA gene; Uvr A h/G-specific adenine glycosylase; synthetic T4 endonuclease V; T4 endo v thymine DNA-glycosylase; Uvr B; Uvr C; nth gene; nfo gene; exonuclease;
                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                           (REGC
                                                                                                                                                                                                                                                                                                                                                                                                         28-MAR-2000;
29-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2001; 2001WO-US09700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA mutation-binding protein; nuclease; DNA mismatch; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli (strain K-12) A/G-specific adenine glycosylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU69755 standard; Protein;
                                                                                                                                                                                                                                                                                                    Cutchen-maloney SL;
                                                                                                                                                                                                                      2001-656920/75.
DB; AAS63242.
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  AAU69737-AAU69760 represent proteins which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LERLEGRFOGLYGVPLFPPEELPGREAAFGVRSR-------PLGEVRHALTHRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRRPKEMMAGLYEFPYIEVEPEEGLQDIEGFTKKMELSLESPLEFLGNLKEQRHAFTNHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACIC-KKVPQCHRCPVRQACGAWRENKQFVLPVRHARKKVIFLHRLVAIVLYDGSLVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATVCLPKRPRCGACPLGAFCRGKEAPGRYPAPRKRRAKE----ERLVALVLL-GRKGVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFKRRAAAVDGNVLRVLSRIFLIETSIDLESTRTWVSRIAQALLPH-KSPEVIAEALIEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLEEVLRVWQGAGYYRRAEHLHRLARSVEE-----LPPSFAELRGLPGLGPYTAAAVASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EALKKWFEKNKRSLPWRDNPTPYSVWVSEVMLQQTRAEVVIDYFNQWMERFPTIESLAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KALLAWYRENARPLPWRGEKDPYRVLVSEVLLQQTRVEQALPYYRRFLERFPTLKALAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFGERVAAVDGNVRRVLSRLFARESPKEKE-----LFALAQGLLPEGVDPGVWNQALMEL
                                                                                                                nuclease
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2000US-0650855
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Pred. No. 8.1e-37;
4; Mismatches 112;
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T4 endo V;
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RESULT 10
AAY09118
ID AAY09
XX AAY09
XX AAY09
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XX AACO
DT 07-JU
XX Adeni
XX Adeni
KW H. py
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                          27-OCT-1997;
                                                                                                                                                                                                                                                                                                                                     Streptococcus
                                                                                                                                                                                                                                                                                                                                                                               Adenine glycosylase; mutY; vaccination; immune response; gastritis; H. pylori infection; stomach cancer; ulcer; gastritis; meningitis; pneumonia; endocarditis; conjunctivitis; sinusitis; bacterial infec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S. pneumoniae adenine glycosylase (mutY) polypeptide
                                                     (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                        06-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY09118 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           synthesis of chimeric proteins comprising a DNA mutation-binding protein, a linker and a nuclease, by recombinant technology. The chimeric proteins are useful for detection, quantification and mapping of DNA sequence variations including mutations, for example, caused by damage and mismatches. The proteins are able to bind to the site of the DNA mutation and cut it out of the molecule. This is used in the invention include cancer and other diseases. The proteins used in the invention include human XPF (or ERCC4), human xeroderma pigmentosum complementation groups A, C and E (XPA, XPC and XPE), human MutS homologue 2 (hMSH2), Serratia marcescens nuclease (Nuc), Thermus thermophilus MutS, Escherichia coli Fapy-DNA glycosylase (Fpg), uracil DNA glycosylase (MutY), synthetic T4 endonuclease V (T4 endo V), endonuclease and accountineases.
                                                                                                                                                                  19-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVSSFTGCMDEGNALWYNLAQPPSVGLAAPVERLLQQ-LRTGAPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGKHFPILDGNVKRVLARCYAVSGWPGKKEVENKLWSLSEQVTPAVGVER--FNQAMMDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -ERLEGRFQGLYGVPLFPPEE-----LPGREAAFGVRSRPLGEVRHALTHRRLRV-----
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                                                                                                          97US-0958676
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Pred. No. 2.5e
61; Mismatches
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2.5e-36;
nes 120;
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Brown JR,

Zalacain

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RESULT 11
ABP27945
ID ABP277
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AC ABP27
XX
DT 02-JU
DT 02-JU
DX
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Strep
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Strep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC This represents a S. pneumoniae adenine glycosylase (mutY) polypeptide. CC MutY can be used to vaccinate patients and raise an immune response against S. pneumoniae by administration of the protein. MutY protein may CC also be applied to implanted devices, wounds or skin to protect against CC or treat S. pneumoniae infections. Administration of mutY polypeptide or the gene will also protect against H. pylori infection which causes CC diseases such as stomach cancer, ulcers and gastritis. Antagonists of CC mutY may be administered to inhibit mutY in an infected individual. CC Diseases such as meningitis, pneumonia, endocarditis, conjunctivitis and CC sinusitis may be diagnosed by detection of mutY gene in an individual by CC RT-CCR, or detecting mutY in a cell sample from a patient. The new mutY protein is expressed by S. pneumoniae at specific stages of infection. It is important for bacterial viability as it contributes to the removal of CC oxidized guanidines from the genome, which can cause mismatches and CC mutations. MutY and the sequences encoding it can therefore be used to CC diagnose or prevent bacterial infections without the use of antibiotics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
 Streptococcus; GAS; GBS; group B
                                Streptococcus polypeptide SEQ
                                                                  02-JUL-2002
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DB; AAX34828.
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                                                                                                                                 standard;
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                                                                                                                                                                                                                                                                                LDVDWLDVCFDTVQHVFSHRKWHVQIVAGQVSDFHDFSDREVRWLSP-EEFKNYPLAKPQ
                                                                                                                                                                                                                                                                                                                                                                             GVHL---ERLEGREQGLYGVPL----FPPEE---LPGREAAFGVRSRPLGE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVASIAFGERVAAVDGNVRRVLSRLFARES----PKEKELFALAQGLLPEGVDPGVWNQA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLATAPEESLLKAWEGLGYYSRVRNMQAAAQQIMTDFGGQFPNTYEGISSLKGIGPYTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALAAASLEEVLRVWQGAGYYRRAEHLHRLARSV-----EELPPSFAELRGLPGLGPYTAA 115
                                                                                                                                                                                                                                                                                                                                             GQFLLEKNESEKLLAGFWHFPFIEVDNFSQEEQFDLFHQVAEESVNSGPSPEESFQQDYD
                                                                                                                                                                                                                                                                                                                                                                                                              LMDLGSDIESPVNPRPEESPVKDFSAAYQNGTMDRYPIKSPKKKPV-PIYLKALVVKNSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                            LMELGATVCLPKRPRCGACPLGAFCRGKE--APGRYP--APRKRRAKEERLVALVLLGRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VISFREKLLAWYDENKROLPWRRSKNPYHIWVSEIMLQQTRVDTVIPYYERFLDWFPTVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 8; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                 377
                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,
                                                                                                                                 Protein;
                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.4%;
                                                                                                                                                                                                                                                                                                              VRHALTHRRLRVEV------RGALWEGEGEDPWKRPLPKLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from Streptococcus pneumoniae useful for diseases such as meningitis, pneumonia a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 465.5; DB 2
Pred. No. 1.1e-35;
                                ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 127;
streptococcus; Streptococcus agalactiae;
                                NO 5066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                374
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                                                                                                                                                                                                                                                                                                                                                                             268
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                                                                                                                                                                                                                                                                                                                                                                                                        CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS C (Streptococcus/GBS (Streptococcus/GAS C (Streptococcus/GBS), given in CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in CC the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and CC antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a CC biological sample. (I) is used to detect Streptococcus in a CC biological sample. (I) is used to determine whether a compound binds to CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by CS treptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity corrections profeins and distinguishing/identifying corrections.
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Best Local :
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24-NOV-2000;
07-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHIR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 3669; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or disease caused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       group A streptococcus; Streptococcus pyogenes; antibacterial;
antiinflammatory; infection; vaccine; meningitis; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
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DB; ABN68576.
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INST GENOMIC
                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                         AVASIAFGERVAAVDGNVRRVLSRLFARE----SPKEKELFALAQGLLPEGVDPGVWNQA 171
                                                                                                                                                                                                                                                                                       NGQYLLEKNTKGRLLGGFWSFPIIETSPLSQQLDLFDDNQSNPIIWQTQNETFEREYQLK
                                 KGVHL--ERLEGR-FQGLYGVPLFPPEELPGREAAF-GVRSRPL---------
                                                                                                                                                                                                   DLADAPEEQLLKAWEGLGYYSRVRNMQKAAQQVMVDFGGIFPHTYDDIASLKGIGPYTAG
                                                                                                                                                                                                                                    ALAAASLEEVLRVWQGAGYYRRAEHLHRLARSVEE-----LPPSFAELRGLPGLGPYTAA 115
                                                                                                LMELGATVCLPKRPRCGACPL----GAFCRGKEAPGRYPAPR-KRRAKEERLVALVLLGR
                                                                                                                                 AIASISFNLPEPAVDGNVMRVMARLFEVNYDIGDPKNRKIFQAIMEILIDPDRPGDFNQA
                                                                                                                                                                                                                                                                     IASFRRTLLEWYDQEKRDLPWRRTTNPYYIWVSEIMLQQTQVNTVIPYYKRFLEWFPQIK
                                                                  LMDLGTDIESAKTPRPDESPIRFFNAAYLNG--TYGKYPIKNPKKKPKPMRIQAFVIRNQ
                                                                                                                                                                                                                                                                                                                                                                                                       384 AA;
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; 2000GB-0028727.
; 2001GB-0005640.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        proteins.
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                                                                                                                                                                                                                                                                                                                                      67;
                                                                                                                                                                                                                                                                                                                                   Score 465; DB 23;
Pred. No. 1.2e-35;
7; Mismatches 125;
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В

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PVSSFTGCMDEGNALWYNLAQPPSVGLAAPVERLLQQ-LRTGAPV 350

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence appears in the specification. The specification describes a human MYH (hMYH) CDNA and protein. The MYH polypeptide of be used for diagnosing cancer, where the decreasing levels of the polypeptide are measured in a sample from a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid of the specification
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                                                                                                                                                                                                                                                                                                                                       FGERVAAVDGNVRRVLSRLFARES-PKEKE----LFALAQGLLPE-GVDPGVWNQALMEL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                         LEEVLRVWQGAGYYRRAEHLHRLARSVEEL-----PPSFAELRGLPGLGPYTAAAVASIA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLDWYDKYGRKTLPWQIDKTPYKVWLSEVMLQQTQVATVIPYFERFMARFPTVTDLANAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLAWYRENAR-PLPWRGEKDPYRVLVSEVLLQQTRVEQALPYYRRFLERFPTLKALAAAS
                                                                              QRPPSGLWGGLYCFPQFADEESLRQWLAQRQIAADNLTQ-LTAFRHTFSHFHLDIVPMWL
                                                                                                                                 -ERLEGREQGLYGVPLFPPEE-----LPGREAAFGVRSRPLGEVRHALTHRRLRV----
                                                                                                                                                                                       GAMICTRSKPKCSLCPLQNGCIAAANNSWALYPGKKPKQTLPERTGTFLLLQHEDEVLLA
                                                                                                                                                                                                                                                                                                  LGKHFPILDGNVKRVLARCYAVSGWPGKKEVENKLWSLSEQVTPAVGVER--FNQAMMDL
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EVRGALWEGEGEDP---WKRPLPKLMEKVLRKALPL: | | | : | : : | | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 464.5; DB
Pred. No. 1.1e-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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В
                            20
                                                                                                                                                                      streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS

(Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS

(Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in

the specification. The proteins have antibacterial and antiinflammatory

activity. (I), nucleic acids encoding (I), ABN66044-ABN71536 and

antibodies that bind (I) are used in the manufacture of medicaments for

the treatment or prevention of infection or disease caused by

Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.

Nucleic acids encoding (I) are used to detect Streptococcus in a

biological sample. (I) is used to determine whether a compound binds to

(I). A composition comprising (I) or a nucleic acid encoding (I), may be

used as a vaccine or diagnostic composition. The disease caused by

Streptococcus that is prevented or treated may be meningitis. Nucleic

acid encoding (I) may be used to recombinantly produce (I) and may be

used in gene therapy. Antibodies to (I) are used for affinity

chromatography, immunoassays, and distinguishing/identifying
                                                                 Query Match
Best Local S
Matches 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 4069; 4525pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-OCT-2000; 2000GB-0026333
24-NOV-2000; 2000GB-0028727
07-MAR-2001; 2001GB-0005640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-352536/38.
N-PSDB; ABN70756.
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                                                                                                                                                              Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for detecting a compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tettelin
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(GENO-) INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-2001;
                                                                                Local Similarity
   7
IASFRETLIGWYDQEKEDLPWERTTNPYYIWVSEIMLQQTQVNTVIPYYKEFLEWFPQIK
                               VEAWRKALLAWYRENARPLPWRGEKDPYRVLVSEVLLQQTRVEQALPYYRRFLERFPTLK
                                                                                                                                374
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Masignani V,
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                                                                                                                                                                proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                     relates to a protein (ABP25413-ABP30895) from group B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide SEQ ID NO
                                                                                                                                AA;
                                                                            27.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    that binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Margarit Ros
                                                                  68;
                                                               Score 461; DB 23;
Pred. No. 2.7e-35;
68; Mismatches 125;
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                                                                                             Length 374;
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61

ALAAASLEEVLRVWQGAGYYRRAEHLHRLARSVEE-----LPPSFAELRGLPGLGPYTAA

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RESULT 14
AAY37104
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28-NOV-1997;
17-DEC-1997;
    AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis;
                                                                                                                                                                         Disclosure; Page 902; 1755pp; English
                                                                                                                                                                                                    Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                  WPI; 1999-371125/31.
                                                                                                                                                                                                                                                                                                                                                                         27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                   10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia trachomatis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY37104 standard; Protein;
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97FR-0015041.
97FR-0016034.
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RESULT 15
ABU01657
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Best Local S
Matches 111
                                                                                                      New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infectio due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or ear infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                   S. pneumoniae type 4 strain protein from coding region
                                                                                                                                                                                                                                                                                                                                                                                                                           11-FEB-2003
                                                                                    Claim 1;
                                                                                                                                                                       WPI;
                                                                                                                                                                                            Masignani V,
                                                                                                                                                                                                                                                27-MAR-2001; 2001GB-0007658
                                                                                                                                                                                                                                                                       27-MAR-2002;
                                                                                                                                                                                                                                                                                            03-OCT-2002
                                                                                                                                                                                                                                                                                                                 WO200277021-A2
                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae type 4 strain
                                                                                                                                                                                                                                                                                                                                                                             Bacterial meningitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU01657;
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                                                                                                                                                                                                                            (CHIR-)
                                                                                                                                                                                                                 (GENO-)
                                                                                                                                                            2003-040579/03.
DB; ABX06945.
                                                                                                                                                                                                                                                                                                                                                                      infection;
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                                                                                   SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
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                                                                                                                                                                                                                                                                                                                                                         therapy;
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Pred. No. 2.7e
19; Mismatches
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The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or

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cc which are the nucleic acid cited above or fragments between nucleotides cc which are the nucleic acid cited above or fragments between nucleotides cc and the sequence not defined in the specification, for amplifying a cc target sequence contained within a Streptococcus nucleic acid sequence. Cc where the first primer is substantially complementary to the target complement of the target sequence, and where the parts of the primers cc complement of the target sequence, and where the parts of the primers cc having substantial complementarity define the termini of the target sequence to be amplified, assay comprising contacting a test compound cc with the protein, and determining whether the test compound the protein and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, cc medicaments for treating or preventing a disease or infection due to streptococcus bacteria, particularly s. pneumoniae, such as pneumonia, stepsies, otitis media or ear infection. They are also useful in developing calentifying immunodominant proteins. The methods are useful for the 1469 proteins expressed by the identified coding regions from the calendaric sequence.
Search completed: September 15, 2003, 13:50:45 Job time : 86 secs
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Matches 123; Conserv
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Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
format directly from WIPO at
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4: sp_human:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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RESULT 1
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Deinococcus radiodurans.";
J. Bacteriol. 183:6151-6158(2001).
EMBL; AE002060; AAF11831.1; -.
EMBL; AF377342; AAL26976.1; -.
HSSP; P17802; IMUN.
TIGR; DR2285; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1."; Science 286:1571-1577(1999).
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                                                                                                                                                                                                                                                                                                                 STRAIN=R1;
MEDLINE=21475757; PubMed=11591657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                              Li X., Lu A.L.; "Molecular Cloning and Functional Analysis of the MutY Homolog
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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MEDLINE=20036896; PubMed=10567266;
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NCBI_TaxID=1299;
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                                          Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F., Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J., Baugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E. Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M., "The Brucella suis genome reveals fundamental similarities between animal and plant pathogens and symbionts."; Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Creat 01-MAR-2003 (TrEMBLrel. 23, Last 01-MAR-2003 (TrEMBLrel. 23, Last A/G-specific adenine glycosylase. MUTY OR BR0493.
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InterPro; IPR001680; WD40.
Pfam; PF00730; HhH-GPD; I1.
SMART; SM00478; ENDO3C; 1.
SMART; SM00525; FES; 1.
SEQUENCE
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Q8G240;
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PROSITE; PS00764; ENDONUCLEASE_III_1;
PROSITE; PS00678; WD_REPEATS_1; 1.

Complete proteome.

SEQUENCE 363 AA; 39388 MW; 1D45C6;
                                  TIGR;
                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-1330 / Biovar 1;
MEDLINE-22247741; PubMed-12271122;
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Brucellaceae; Brucella.
NCBI_TaxID=29461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    VEV----YRAEADRP-RQPVRGAALSRLDHKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKREGSLLGGLFGLPL - - - EEIGARETAADALARLQARLGAEVKECLGTVQHGMTHRRLS
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        WW.
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                                                                                                                                                                                                                                                                                                                                          Created)
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Pred. No. 4.7e-42;
8; Mismatches 96
        E147F8C3CEDB74E7 CRC64
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Best Local S
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Best Local S
Matches 134
                                                                                                                                                                                          InterPro; IPR004035; EndoIII_FCL.
InterPro; IPR003265; Endo_3c.
InterPro; IPR003651; Fes_bind.
InterPro; IPR003651; MutY.
Pfam; PF00730; HhH-GPD; 1.
SMARR; SM00478; ENDO3C; 1.
SMARR; SM00525; FES; 1.
INTERPAMS; TIGR01084; mutY; 1.
PROSITE; PS00764; ENDONUCLEASE_III_1; 1.
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MEDLING=20020109; PubMed=11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Rez Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson Haselkorn R., Kyrpides N., Overbeek R.;
"The genome sequence of the facultative intracellular path Brucella melitensis."; U.S.A. 99:443-448(2002).
EMBL, AED09581; AAL52623.1; C. TERDOLOGE SALTT ECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brucella melitensis.
Bacteria; Proteobacteria;
                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brucellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8YFS8
                                                                                                                                                                        Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=29459;
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                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMMDLGATICTPRRPACALCPLNKGCIALCERDPEDFPVKAPKAEKPVRTGAAFIAIAGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAAIAAIAFGEQVAVVDGNVERVISRLYAIDTPLPVAKAQICALMGQMTPPD-RPGDFAQ
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  LLAWYRENARPLPWR - -
                                                                                                                                                   Glycosidase; Complete proteome. 375 AA; 40938 MW; 2F5FD3E76533B46D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                   Conservative
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                                                                        32.4%;
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38.4%; Pred. No. 2.4e-33;
Live 53; Mismatches 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alphaproteobacteria;
                                              Score 551.5;
Pred. No. 3.1e
33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -LAGMTEVPGSGWTARIDGDATVNAAPFSAAWTPSGTITHVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
  -GE-KDPYRVLVSEVLLQQTRVEQALPYYRRFLERFPT
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                                                                                                  DB 16;
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                                                   51;
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Best Local
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InterPro; IPRO04035; Endo_III_FCL.
InterPro; IPRO03265; Endo_3c.
InterPro; IPRO03651; FeS_bind.
InterPro; IPRO03651; FeS_bind.
InterPro; IPRO05760; MutY.
Pfam; PF00633; HHH; 1.
Pfam; PF00730; HhH-GPD; 1.
SMART; SM00525; FES; 1.
SMART; SM00525; FES; 1.
TIGRFAMS; TIGR01084; mutY; 1.
PROSITE; PF007764; ENDONUCLEASE_III_1; 1.
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Q92RF0;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Probable A/G-specific adenine glycosylase protein.
MUTY OR R00928 OR SWC00452.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Capela D., Barloy-Hubler F., Golzy J., Bothe G., Ampe F., Batut Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL; AL591785; CAC45500.1; -.
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LKALAAASLEEVLRVWQGAGYYRRAEHLHRLARSVE---
                                                 LLEWYDRHHRDLPWRVPPAAARKGAVADPYRVWLSEVMLQQTTVQAVKAYFEKFLALWPT
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                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                              39944 MW;
                                                                                                                                                                                 31.2%; Score 531; DB 1 37.6%; Pred. No. 1e-31;
                                                                                                                                                                                                                                                              698224AA25089831 CRC64;
                                                                                                                                                         Mismatches
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Pfam; PF00730; HhH-GPD; 1.

SMART; SM00478; ENDO3c; 1.

SMART; SM00525; FES; 1.

TIGRFAMS; TIGR01084; mutY;
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=ATCC 19089 MEDLINE=21173698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003265;
InterPro; IPR003651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caulobacteraceae; Caulobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caulobacter crescentus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AE005710; AAK22364.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AG
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                   DALRSALLAWYDAQARDLAWRVGPAERRAGVRSDPYRVWLSEVMLQQTTVPHATPYFLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VFTHFELHLSVFRARVGRADIGEARTDTSGWWEPLASLRAQALPTVMKKAIAKAIPHAFE
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                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000445; HhH.
IPR005760; Muty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteobacteria; Alphaproteobacteria; Caulobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   366
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                                                                                                                                                                                                                                   AΑ;
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PubMed=11259647;
                                                                                                                                                                                                                                   37615 MW;
                                                                                                                                                30.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endo_3c.
FeS_bind
                                                                                                                                                                                                                                                                                 mutY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -QGLYGVPLFPPEELPGRE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence up
                                                                                                                     Score 520; DB 16;
Pred. No. 6.3e-31;
3; Mismatches 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                   DD96F16FB2A4ABC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349
                                                                                                                                                                               DB 16;
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on update)
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           SMART; SM00478; ENDO3C; 1.
SMART; SM00525; FES; 1.
TIGREAMS; TIGR01084; mutY;
PROSTTE: PROSTTE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo I Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Kutyavin C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8UH85;
                                                                                                                                                                                                                                                                                                                                                                                                      Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-21608550; PubMed-11743193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agrobacterium tumefaciens (strain C58 / ATCC 33970)
Bacteria; Proteobacteria; Alphaproteobacteria; Rhiz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A/G-specific adenine glycosylase. MUTY OR ATU0798 OR AGR_C_1460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TREMBLrel. 21, 01-JUN-2002 (TREMBLrel. 21, 01-MAR-2003 (TREMBLrel. 23,
                                                                                                                                                                                                                                                                                                                             "Genome sequence of the plant pathogen Agrobacterium tumefaciens C58.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-21608551;
                                                                                                                                                                                                                                                                                                    Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                     Cielo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome
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                                                                                                            Pro; IPR005760; Muty. PF00730; HhH-GPD; 1.
                                                                                                                                                                                                                                             AE009046; AAL41814.1; -. AE008012; AAK86607.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTHFSLTLRVFAADGANDGDFVWTPREGLGALPSVFLKAAMAAQRLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLTRGDEVALVRRPPKGLLGGMLGLPTSDWRTASYDDAEAVA - AAPLAAAWRDLGAVEHV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TQRWPTVLDLAAVEDGDLMAAWAGLGYYARARNLLACARAVANDHGGVFPGTEEGLRALP
                                                                                                                                   IPR004035; EndoIII_FCL.
IPR003265; Endo_3c.
IPR003651; FeS_bind.
IPR005760; MutY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .; PubMed-11743194;
     ENDONUCLEASE_III_1;
                                 mutY; 1
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Perry M.,
Dolan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       ₩.,
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Matches
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Best Local
                      Query Match
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                                                                                          DNA Res. 7:331-338(2000).

EMBL; AP003012; BAB53965.1; -

InterPro; IPR004035; EndoIII_
InterPro; IPR003265; Endo_3c.

InterPro; IPR003651; Fes_bind
InterPro; IPR003651; MutY.

Pfam; PR00730; HhH-GPD; 1.

SMART; SM00478; ENDOSc; 1.

SMART; SM00525; FES; 1.
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                                                                                                                                                                                                                          Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasar Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kiura Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsunot Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto Takeuchi C., Yamada M., Tabata S.;
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01-OCT-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                STRAIN-MAFF303099;
                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Alphaproteobacteria; Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                    "Complete genome structure Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                     MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                              Phyllobacteriaceae;
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                        Length 396;
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Best Local
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Q8DJZ3; Q1-MAR-2003 (TrEMBLrel. 2
Q1-MAR-2003 (TrEMBLrel. 2
Q1-MAR-2003 (TrEMBLrel. 2
Q1-MAR-2003 (TrEMBLrel. 2
Adenine glycosylase.
TLL1077
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Makamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
DNA Res. 9:133-130(2002).
EMBL; AP005372; BAC08630.1; -.
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                                                           ELGATVCLPKRPRCGACPLGAFCRG-----KEAP---GRYPAPRKRRAKEERLVALVLL
                                                                                                                                                                                                                                                                                     AWRKALLAWYRENARPLPWRGEKDPYRVLVSEVLLQQTRVEQALPYYRRFLERFPTLKAL
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368 AA;
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                      DLGATICTPRHPLCHACPWQHHCLAHRHQLTHEIPRKMSRSPLPHKKIG----
                                                                                                     LSAAFNQPQPILDGNVKRVLARLYGLTVPPKQAEAQLWQWSAQLLCPQ--SPRDFNQALM
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23,
                                                                                                                                                                                                                                                                                                                                               43; Mismatches 102;
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Pred. No. 8.8e-30;
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Pfam; PF00730; HhH-GPD; 1.
SMART; SM00478; ENDO3C; 1.
SMART; SM00525; FES; 1.
TIGRFAMS; TIGR01084; MULY; 1.
PROSITE; PS00764; ENDONUCLEASE_III_1; 1.
Hydrolase; Glycosidase; Complete protecome.
SEQUENCE 349 AA; 39560 MW; BB0EF134613A1A49
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Adenine glycosylase (EC 3.2.2.-).
MUTY OR NMA1614.
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EMBL; AL162756; CAB84842.1;
HSSP; P17802; 1MUN.
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InterPro; IPR003265; Endo_3c.
InterPro; IPR003551; Fes_bind.
InterPro; IPR00345; HhH.
InterPro; IPR005760; MutY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=22491 / Serogroup
MEDLINE=20222556; PubMed-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; Betaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       meningitidis 22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                          ER--LEGREQGLYGVPLEPPEELPGRE---AAFGVRSRPLGE---VRHALTHRRLRVEVR
                                                                                        GATYCLPKRPRCGACPLGAFCRGKEAPGRYPAPRKRRAKEE---RLVALYLLGRKG-VHL
                                                                                                                                        FURRETILDGNVKRYLCRVFARDGNPQDKKFENSLWTLAESLLPSENADMPAYTQGLMDL
                                                                                                                                                           LIRWQKQHGRHHLPWQ-VKNPYCVWLSEIMLQQTQVATVLDYYPRFLEKFPTVQTLAAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAYTHFRVTLHV
                                                           GATVCKRTKPLCHQCPMADICEAKKQNRTAELPRKKTAAEVPTLPLYWLIVRNRDGAILL
                                                                                                                                                                                                                       QDEVLSLWAGLGYYSRARNLHKAAQQVVEQFGGTFPSERKDLETLCGVGRSTAAAICAFS
                                                                                                                                                                                                                                                              LEEVLRVWQGAGYYRRAEHLHRLARSVEE-----LPPSFAELRGLPGLGPYTAAAVASIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRKGVHLERL--EGREQGLYGVP---LFPPE---ELPGRE--AAFGVRSRPLGE----VR
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rogroup A / Serotype
PubMed=10761919;
                                                                                                                                                                                                                                                                                                                                                                                                  29.68;
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                                                                                                                                                                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                                                                                                                                                                                  Score 503; DB
Pred. No. 1.2e
52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               349
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                                                                                                                                                                                                                                                                                                                                                                                  DB 16;
L.2e-29;
mes 111;
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Holroyd

36;

Gaps

132

121

72

192

231

283 252

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RESULT 10
OJ158
AC OJ158
AC OJ158
DT 01-JA
DT 01
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Submitted
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O31584;
O1-JAN-1998
O1-JAN-1998
O1-MAR-2003
                                                                                                                                                                                                                                                         degrees-81
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-97101647; PubMed-8946165;
                                                    InterPro;
                                                                                                                                                                                                                                      Yamamoto H., Uchiyama S., Sekiguchi J.;
"Cloning and sequencing of a 27.8-kb nucleotide sequence of the
degrees-81 degrees region of the Bacillus subtilis genome contai
                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Bacteria; Firmicutes;
NCBI_TaxID=1423;
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                                                                                                                                                                                              Res.
                                                                                                     299108; CAB12691
D85082; BAA24483
P17802; IMUY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         390:249-256(1997).
                                                                                                                                                                                        locus.";
3:257-262(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM N.A
                     IPR000445;
                                              IPR003651;
                                                                                                                                                                                                                                                                                                                                                                                                                               Ogasawara N., (NOV-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GALW--EGEGEDPWKRP-----LPKLME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAQMPSESPSDGIWIKPAHLKDYGLPKPLE 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKRPAKGIWGGLYCVPCF--ESLNGLSDFAAKFSLTMADMDEQTALTHRLTHRLLLITPF 310
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                                                                                                                                 BAA24483.1; -.
                                       Endo_3c.
FeS_bind.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Yoshikawa
the EMBL/G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05,
23,
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EMBL/GenBank/DDBJ
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Last sequence update)
Last annotation updat
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Q92F41
         ALD DE COMPANDA ALD DE COMPAND
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Best Local
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                                 SEQUENCE FROM N.A.

MEDLINE-98445380; PubMed-9770495;

Kroll J.S., Wilks K.E., Farrant J.L., Langford P.R.;

Kroll J.S., Wilks K.E., Farrant J.L., Langford P.R.;
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINB=98084476; PubMed=9423860;
Wilks K.E., Dunn K.L., Farrant J.L
Langford P.R., Kroll J.S.;
"Periplasmic superoxide dismutase
Infect. Immun. 66:213-217(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9ZF41;
01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                              pathogens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                           Microbiology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adenine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria
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   Acad.
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Sci.
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U.S.A.
                                                                                                                                                                                                                                                                                                                      Farrant J.L.,
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InterPro; IPR005760; Muty.
Pfam; PF00633; HHH; 1.
Pfam; PF00730; HhH-GPD; 1.
SMART; SM00478; END03c; 1.
SMART; SM00525; FES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMs; TIGR01084; mutY;
                                                                                                                                                                                                                                                                                                                                                    1 VEAWRKALLAWYRENARPLPWRGEKDPYRVLVSEVLLQQTRVEQALPYYRRFLERFPTLK
    QVYIHKRPSKGLLANLW-----
                                                                                                                    LMELGATVCLPKRPRCGACPLGAFCRGKEAPGRYPAPRKRRAKE---
                                                                                                                                                       AVLSIAYNKPIPAVDGNVMRVMSRILSIWDDIAKPKTRTIFEDAIRAFISKEKPSEFNQG
                                                                                                                                                                                  AVASIAFGERVAAVDGNVRRVLSRLFA----RESPKEKELFALAQGLLPEGVDPGVNNQA 171
                                                                                                                                                                                                                                    ALADADEEKVLKAWEGLGYYSRVRNLQSAVKEVKQEYGGIVPPDEKDFGGLKGVGPYTKG
                                       ---VHLERLEGREQGLYGVPLFPPEELPGREAAFGVR------
                                                                                                                                                                                                                                                                         ALAAASLEEVLRVWQGAGYYRRAEHLHRLARSVEE----LPPSFAELRGLPGLGPYTAA 115
                                                                                                                                                                                                                                                                                                               IQQFRDDLISWFEREQRVLPWREDQDPYKVWVSEVMLQQTRVETVIPYFLRFVEQFPTVE
                                                                            LMELGALICTPKSPSCLLCPVQQHCSAFEEGTERELPVKSKKKKPGIKTMAAIVLTDEDG
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· EFPNLETQKGIKTEREQLIAFLENEYGIQADISDL
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No. 1.6
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                                         SRP
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SEQUENCE FROM N.A.
MEDLINE-96118708; PubMed-7496539;
Kroll J.S., Langford P.R., Wilks K.E., Keil A.D.;
"Bacterial [Cu,Zn]-superoxide dismutase: phylogen eukaryotic enzyme, and not logy 141:2271-2279(1995). Proteobacteria; ceae; Neisseria. Betaproteobacteria; Neisseriales Last Last Created) PRT; sequence up so 346 e: phylogenetically distinct rare after all!"; A update) update)

95:12381-12385(1998)

and Neisseria:

in

Reddin K.M.,

Gorringe A.R.,

meningococcal pathogenicity.";

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RESULT
Q9JYW9
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INTERPRO; IPRO04035; EndoIII_FCL.

InterPro; IPR003265; Endo_3c.

R InterPro; IPR003651; FeS_bind.
R InterPro; IPR003651; FeS_bind.
R InterPro; IPR005760; Mutv.
R Pfam; PF00633; HHH; 1.

PF4nn; PF00730; HhH-GPD; 1.

NR Pfam; PF00730; HhH-GPD; 1.

NR SMART; SM00478; ENDO3c; 1.

DR SMART; SM00525; FES; 1.

DR TIGRPAMS; TIGR01084; mutv; 1.

DR PROSITE; PS00764; ENDONUCLEASE_III_1; 1.

PROSITE; PS00764; ENDONUCLEASE_III_1; 1.

CROTTENCE 346 AA; 39230 MW; 00AF2A26BEBEC3A1 CRC64;
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Best Loc
Matches
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update
01-MAR-2003 (TrEMBLrel. 23, Last annotation upda
A/G-specific adenine glycosylase.
NMB1396.
Nelsseria meningitidis (serogroup B).
Bacteria; Proteobacteria; Betaproteobacteria; Ne
                                                             Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson Elsen J.A., Ketchum K.A., Hood D.W., Pederson J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Pederson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-MC58 / Serogroup B;
MEDLINE-20175755; PubMed-10710307;
                 "Complete genome MC58.";
Science 287:1809-
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P17802; 1
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287:1809-1815(2000).
E002488; AAF41760.1;
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Pred. No. 2.7e-29;
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InterPro; IPR004035; EndoIII_FCL.

DR InterPro; IPR003265; Endo_3c.

DR InterPro; IPR003615; FeS_bind.

DR InterPro; IPR003615; HhH.

DR InterPro; IPR004615; Muty.

DR Pfam; PF0033; HHH; 1.

DR Pfam; PF00633; HHH; 1.

DR Pfam; PF00730; HhH-GPD; 1.

PR SMART; SM00478; ENDO3c; 1.

PR SMART; SM00478; ENDO3c; 1.

R TIGRFAMS; TIGR01084; muty; 1.

R PROSITE; PS00764; ENDONUCLEASE_III_1; 1.

Complete Proteome.

SEQUENCE 349 AA: 30007.
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Bacillus h
Bacteria;
InterPro;
InterPro;
InterPro;
InterPro;
                                      "Complete genome sequence of the alkaliphilic bacterium I halodurans and genomic sequence comparison with Bacillus Nucleic Acids Res. 28:4317-4331(2000).
EMBL; APO01510; BAB04650.1; -.
                                                                                                     SEQUENCE FROM N.A.
STRAINC-125 / JCM 9153;
STRAINC-125 / JCM 9153;
MEDLINE-20512582; PobMed-11058132;
Takami H., Nakasone K., Takaki Y.,
Takami F., Hirama C., Nakamura Y., O
                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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           IPR004035;
IPR003265;
IPR003651;
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Pred. No. 2.7e-29;
2; Mismatches 112;
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Ogasawara
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annotation updat
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Matches 122
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SEQUENCE
                                                                                                                                       MEDLINE-22220767; PubMed-12235376;
Takami H., Takaki Y., Uchiyama I.;
Takami esequence of Oceanobacillus iheyensis isolated from
Ridge and its unexpected adaptive capabilities to extreme
environments.";
                                                                                                                                                                                 SEQUENCE FROM N.A.

CTRAITN-HTEB31 / DSM 14371 / JCM 11309;

CTRAITN-HTEB31 / DSM 14371 / JCM 11309;
                                                                                                                                                                                                                                                                                                                    Q8CV61;
                                                                                                                EMBL; AP004596; BAC12852.1;
                                                                                                                                                                                                                               Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales;
NCBI_TaxID-182710;
                                                                                                                             Nucleic Acids Res.
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Pfam; PF00730; HhH-GPD; 1.
SMART; SM00478; ENDO3C; 1.
SMART; SM00525; FES; 1.
SMART; SM00278; HhHI; 1.
TIGRFAMS; TIGR01084; mutt; 1.
PROSITE; PS00764; ENDONUCLEASE_III_1;
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InterPro; IPR005760;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                          proteome.
354 AA;
           VEAWRKALLAWYRENARPLPWRGEKDPYRVLVSEVLLQQTRVEQALPYYRRELERFPTLK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
IPVFQTDLLEWYYLNKRDLPWRREPNPYKTWVSEIMLQQTKVDTVIPYFNRFMEKYPTVY
                                                                                                                                                                                                                                                                                                                                                                                                                              QVLIERRPEKGLLAKLWQFPNVELESTKNAQQVLGDYIHERFHLDAAVGEYVQTVEHVFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -VHLERL--EGRFQGLYGVPLFPPEELPGREAAFG--VRSR-----PLGE----VRHALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LMELGATVCLPKRPRCGACPLGAFCRGKEAPGRYPAP---RKRRAKEERLVALVLLGRKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AILSIAYDQPEPAVDGNVMRVLSRVLYIEEDIAKVKTRTLFESLLYDLISKENPSFFNQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALAAASLEEVLRVWQGAGYYRRAEHLHRLARSV-----EELPPSFAELRGLPGLGPYTAA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteome.
372 AA; 42538 MW; 1AA0118DC5177EB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     HLIWNIRVYEATVKG-----VPSLNDK
                                                                                                                                                                                                                                                                                                                                                                                                          HRRLRVEVRGALWEGEGEDPWKRPLPKLMEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LMELGALVCTPTSPGCLLCPVRDHCRAFAAGVQEQLPIKAKKKKPKAKQLIAAVIRNEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISTFONDLYTWFSNHYRELPWRENKDPYRVWVSEIMLOOTRVDTVIPYYOAFMROFPTLE
                                              Conservative
                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                          30:3927-3935(2002).
                                                                                          41235 MW;
                                                         29.0%;
                                                                                                                                                                                                                                                                         glycosylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HHH_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54;
                                                                                                                                                                                                                                                                                  Last sequence up
                                                                                                                                                                                                                                                                                                         Created)
                                            Score 492.5; DB 16
Pred. No. 7.2e-29;
2; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3.2e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 497.5;
                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                         76296B9FFB1AAB1B CRC64;
                                                                                                                                                                                                                                        Oceanobacillus
                                                                                                                                                                                                                                                                                                                                354
                                                                                                                                                                                                                                                                                                                                                                                                          305
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                                                                                                                                                                                                                                                                                                                               Ą
                                                                                                                                                                                                                                                                                                                                                                                     331
                                                                  DB 16;
                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120;
                                                                                                                                                                                                                                                                                  update)
                                            Indels
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                                                                Length
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                                                                    354;
                                           19;
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                                           Gaps
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 69
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Q9CH97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
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                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00633; HHH; 1.

Pfam; PF00730; HhH-GPD; 1.

SMART; SM00478; ENDO3C; 1.

SMART; SM00525; FES; 1.

SMART; SM00525; FES; 1.

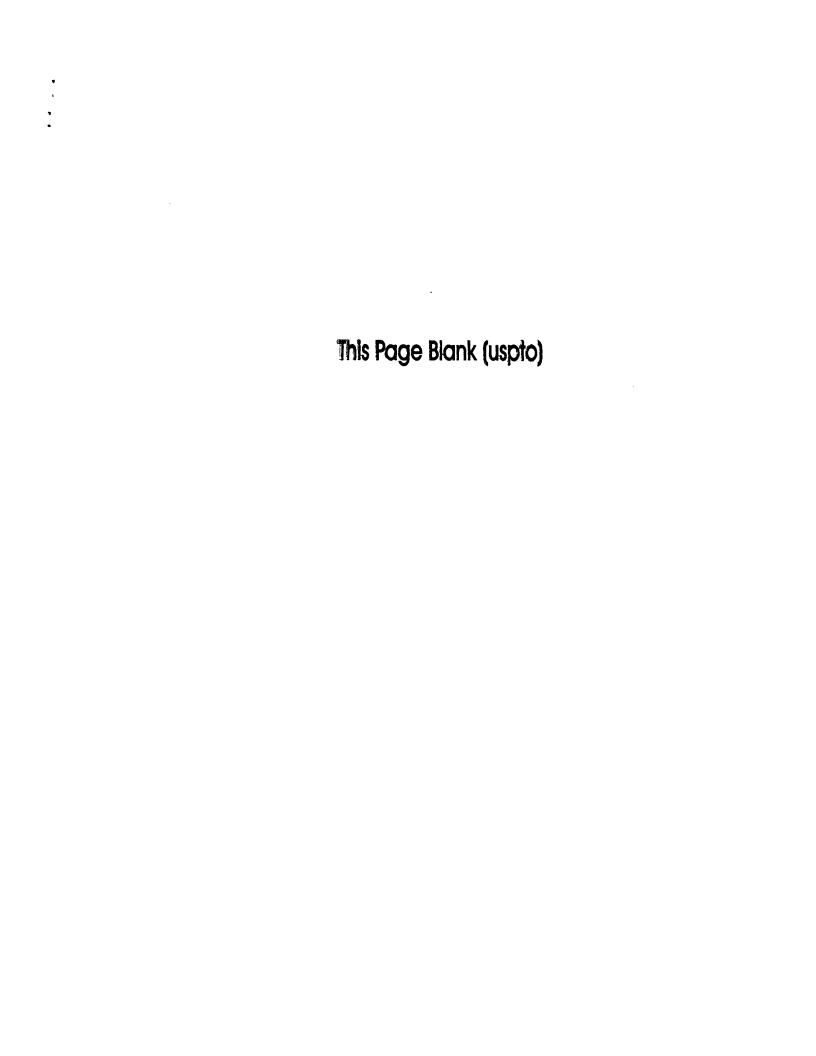
IGRAMS; TIGRO1084; mutt; 1.

PROSITE; PS00764; ENDONUCLEASE_III_1; 1.

Complete proteome.

SEQUENCE 387 AA; 44220 MW; 48C56C24E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9CH97 PRELIMINAKI; Q9CH97; Q9CH97; Q9CH97; Q9CH97; Q9CH97; Q1-JUN-2001 (TrEMBLrel. 17, Created) Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update) Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update) Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004035; InterPro; IPR003265; InterPro; IPR003651; InterPro; IPR00445; InterPro; IPR003583; InterPro; IPR003583; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE006318; AAK04939.1; HSSP; P17802; 1MUN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21235186; PubMed=11337471;
Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactococcus lactis (subsp. lactis) (Streptococcus lactis) Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                     116
                                                                                                                                                                                                                                                                                                                                  108;
                                                                                                           8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188
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                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                AVASIAFGERVAAVDGNVRRVLSRLFARE----SPKEKELFALAQGLLPEGVD---PGVW 168
                                                                                                                                       ALAAASLEEVLRVWQGAGYYRRAEHLHRLARSVEE-----LPPSFAELRGLPGLGPYTAA
                                                                                                                                                                                                                                                     proteome.
387 AA; 44220 MW; 48C56C24D1B76A71 CRC64;
AIASISFGLAEPAIDGNLMRVTSRLFELDCDISKSSSRKIF---DGYLRKLISKKRPGDF
                                                                                                        TLAQADDAELLKLWEGLGYYSRARNLKIAAQEVVDKYNGKFPDNLADILSLKGIGPYTAA
                                                                                                                                                                                                                 IKEFQQDLLSWYDDNKKPLPWRKTTEPYKIWISEIMSQQTQVETVMPYYERFMKKYPTIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QAIMDLGATICTPKKPTCMFCPVMEHCQAFQHGIQEQLPIKKKAKKQKIKQYVVLLIRND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVASIAFGERVAAVDGNVRRVLSRL-----FARESPKEKELFALAQGLLPEGVDPGVWN 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALAAASLEEVLRVWQGAGYYRRAEHLHRLARSV-----EELPPSFAELRGLPGLGPYTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QGEYVIEKRSDQGLLANLWQFPMVPLDEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AILSIAFNQPVPAVDGNVLRVFSRILQIEDDIAKQSTK-KEIEQYV-GEIISHQDPSSFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLAKADEQDVLKSWEGLGYYSRARNLQTAVREVVDTYNGEIPNNEKELASLKGIGPYTKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR003583; HHH_1.
IPR005760; Muty.
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                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                        28.9%;
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FeS_bind.
HhH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EndoIII_FCL.
                                                                                                                                                                                                                                                                                                                                  57;
                                                                                                                                                                                                                                                                                                                         Pred. No. 8.76
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                     Score 492; DB 16;
Pred. No. 8.7e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276
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                                                                                                                                                                                                                                                                                                                               84;
                                                                                                                                                                                                                                                                                                                                                                               Length 387;
                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lactis).
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                                                                                                                                                                                                                                                                                                                               26;
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                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                   67
184
                                                                                                     127
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Search (Job time	Db	Qy	DЬ	Qy
Search completed: September 15, 2003, 13:53:00 Job time : 101 secs	243 ENSLGETYLEKRPSKGLLADMWTFPLTELPAAD 275	224 LGRKG-VHLERLEGREQGLYG-VPLEPPEELPGRE 256	185 NQALMDLGSLVCSPKSPKCEACPLLNYCAAAASGKQLNYPVKTKKIKQKDLYFTAFAL 242	169 NQALMELGATVCLPKRPRCGACPLGAFCRGKEAPGRYPAPRKR-RAKEERLVALVL 223



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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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           on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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MUTY_ECOLI STANDARD; PRT; 350
P17802;
01-AUG-1990 (Rel. 15, Created)
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A/G-specific adenine glycosylase (EC 3.2)
MUTY OR MICA OR B2961.
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                                                                     MEDLINE-91161503; PubMed-2001994;
                                                                                                                                                 MEDLINE-90326504; PubMed-2197596; Michaels M.L., Pham L., Nghiem Y., Cr "Muty, an adenine glycosylase active endonuclease III."; Crendonuclease III.";
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Enterobacteriaceae; Escherichia.
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Pfam; PF00633; HHH; 1
SMART; SM00478; ENDO3G; 1.
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SMART; SM00525; H5H; 1
TIGRFAMS; TIGR01084; mutt; 1.
PROSITE; PS01764; ENDONUCLEASE_III_1; 1.
PROSITE; PS01764; ENDONUCLEASE_III_1; 1.
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Pfam; PF00730; HHH; 1
SMART; SM00478; END03C; 1.
SMART; SM00525; FES; 1.
SMART; SM00525; FES; 1.
SMART; SM00525; FES; 1.
TIGREAMS; TIGR01084; MULT; 1.
PROSITE; PS00764; ENDONUCLEASE_III_1; 1.
DNA repair; Hydrolase; Glycosidase; Iron
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Interpro: IPR004035; EndoIII_FCL.
Interpro: IPR004035; EndoIII_HhH.
Interpro: IPR003651; Fes_bind.
Interpro: IPR003651; Fes_bind.
Interpro: IPR003593; HHH_1.
Interpro: IPR003593; HHH_1.
Interpro: IPR003593; HHH_1.
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PDB; 1MUD; 29
PDB; 1MUV; 26
PDB; 1MUV; 26
PDB; 1KG2; 26
PDB; 1KG3; 2
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WEDLINE-99061333; PubMed-9846876;
Guan Y., Manuel R.C., Arvai A.S., Parikh S.S., Mol C.D., Miller J.H.,
Lloyd S., Tainer J.A.,
"Muty catalytic core, mutant and bound adenine structures define
specificity for DNA repair enzyme superfamily.";

SPECIAL STRUCT. BIOL. 5:1058-1064 (1998).
-i- FUNCTION: ADENINE GLYCOSYLASE ACTIVE ON G-A MISPAIRS. MUTY ALSO
CORRECTS ERROR-PRONE DNA SYNTHESIS PAST GO LESIONS WHICH ARE DUE
TO THE OXIDATIVELY DAMAGED FORM OF GUANINE: 7,8-DIHYDRO-8-
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Blatther F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhaw G.F., Mau B., Shao Y., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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MEDLINE-97426617; Pu
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"Nucleotide sequence of the Escherichia coli micA gene required A/G-specific mismatch repair: identity of micA and muty.";
Bacteriol. 173:1902-1910(1991).
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COFACTOR: BINDS A 4FE-4S CLUSTER WHICH IS NOT IMPORTANT FOR THE CATALYTIC ACTIVITY, BUT WHICH IS PROBABLY INVOLVED IN THE POSITIONLING OF THE ENZYME ALONG THE DNA STRAND.

SIMILARITY: BELONGS TO THE NTH/MUTY FAMILY.
                                         proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete genome sequence of Escherichia coli K-12.";
nce 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                    EG10627;
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26-AUG-99
26-NOV-02
26-NOV-02
26-NOV-02
26-NOV-02
26-NOV-02
26-NOV-02
26-NOV-02
10-APR-02
                                    Hydrolase; Glycosidase; Iron-sulfur; 4Fe-4S;
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                    192
IRON-SULFUR (4FE-4S)
                              3D-structure;
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304 281 В γQ B δ В δÃ 밁

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RESULT 2
ID MUTY_E
AC P17802
D1 -AUG
D7 01-AUG
D7 15-SEP
DE A/G-SP
GN MUTY 0
OS Escher
OC Entero
OX NCBI_T
RP SEQUEN
RX MEDLIN
RA MICChae
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RT Nuclei
RN [2]
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RT SEQUEN
RX MEDLIN

STRAIN-K12

SEQUENCE FROM N.A

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MUTY_HAEIN
ID MUTY_H
AC P44320
DT 01-NOV
DT 28-FEB
DE A/G-sp
GN MUTY_O
SH HAEMOP
OC Bacter
OC Pasteu
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Best Local :
                                      MUTY_HAEIN STANDARD
P44320;
01-NOV-1995 (Rel. 32, C
01-NOV-1995 (Rel. 32, L
20-FEB-2003 (Rel. 41, L
A/G-specific adenine 91
MUTY OR HI0759.
              Haemophilus influenzae.
Bacteria; Proteobacteria;
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  Pasteurellaceae; Haemophilus
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                                                                                                                                                                                           PVSSFTGCMDEGNALWYNLAQPPSVGLAAPVERLLQQ-LRTGAPV
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Last annotation
Quycosylase (EC 3
                                                     glycosylase
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            Gammaproteobacteria;
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STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
MEDLINE-95350630; PubMed-7542800;
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; C64091; C64091.
P; P17802; IMUY.
R; H10759; -
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InterPro; IPR003265; Endo_3c.

R InterPro; IPR004035; EndoIII_FCL.

R InterPro; IPR004035; EndoIII_HhH.

R InterPro; IPR003651; FeS_bind.

R InterPro; IPR003651; FeS_bind.

R InterPro; IPR005760; Mutr.

R InterPro; IPR005760; Mutr.

R Pfam; PF00730; HHH; 1.

R Pfam; PF00633; HHH; 1.

R Pfam; PF00633; HHH; 1.

R Pfam; PF00633; HHG; 1.

R Pfam; PF00633; HHG; 1.

R Pfam; PF00634; ENDONGCLEASE_III_1; 1.

R PROSITE; PS00155; ENDONGCLEASE_III_2; 1.

DNA repair; Hydrolase; Glycosidase; Iron-sulfur; 4Fe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SIMILARITY: BELONGS TO THE N'HAMUTY FAMILY.
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European Bioinformatics Institute.
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SVLNQPYPILDGNVKRVLARYFAVEGWSGEKKVENRLWALTEQVTPT-TRVADFNQAMMD
                                                                                                           KALLAWYRENARP-LPWRGEKDPYRVLVSEVLLQQTRVEQALPYYRRFLERFPTLKALAA
                                                     IAFGERVAAVDGNVRRVLSRLFA----RESPKEKELFALAQGLLPEGVDPGVWNQALME
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                                                                                                                                                                                                                                                                                                                                            Score 445; DB Pred. No. 1.3e 59; Mismatches
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IRON-SULFUR (4FE-4S) (BY SIMILARITY).
IRON-SULFUR (4FE-4S) (BY SIMILARITY).
IRON-SULFUR (4FE-4S) (BY SIMILARITY).
; C443F625131B2A21 CRC64;
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J.L., Geoghagen N.S.M.,
V., Fraser C.M., Smith H.O.,
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                                                                                                                                                                                                                                                                                                                                                                       DB 1;
.3e-27;
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Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA
COllins M., Connor R., Cronin A., Davis P., Feitwell T., Eraser A.,
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Collins M., Connor R., Cronin A., Davis P., Feitwell T., Eraser A.,
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Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
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James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
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Colliver K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E.,
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Colliver K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E.,
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Colliver K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E.,
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Colliver K., Cyllor R., Filtz C., Holzer E.,
RA
Colliver K., Cyllor S., Lehrach H., Reinhardt R., Pohl T.M.,
RA
Colliver K., Caddeu E., Draano S., Cloux S., Lelaure V., Mottler S.,
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Colliver K., Caddeu E., Draano S., Cloux S., Lelaure V., Mottler S.,
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Colliver K., Caddeu E., Draano S., Cloux S., Lelaure V., Mottler S.,
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Colliver K., Caddeu E., Draano S., Cloux S., Lelaure V., Mottler S.,
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Colliver K., Caddeu E., Draano S., Cloux S., Lelaure V., Mottler S.,
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Colliver K., Caddeu E., Draano S., Cloux S., Lelaure V., Mottler S.,
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Colliver K., Caddeu E., Callard R., Parlade V.A.
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MEDLINE-98411305; PubMed-9737967;

Lu A.-L., Fawcett W.P.;

"Characterization of the recombinant Muty homolog, an adenine DNA 91/905/lase, from yeast Schizosaccharomyces pombe.";

J. Biol. Chem. 273:25098-25105(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21848401; PubMed-11859360; Wood V., Gwilliam R., Rajandream W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4896
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sen the Swiss Institute of Bio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVRGALWEGEGEDPWKRPLPKLME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERLE--GRFQGLYGVPLFPPE----ELPGREAAFGVRSRPLGEVRHALTHRRLRV-----
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               jht. It is produced
Bioinformatics and
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through a collaboration d the EMBL outstation -
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UTY_BUCAP

ID MUTY_BUCAP

ID MUTY_BUCAP

AC QBK926;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE A/G-specific adenine glycosylase (EC 3.2.2.-)

MUTY OR BUSG534.
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R InterPro; IPR004365; Endo_3c.

R InterPro; IPR004365; EndoIII_FCL.

R InterPro; IPR004365; EndoIII_HhH.

R InterPro; IPR004365; EndoIII_HhH.

R InterPro; IPR00446; HhH.

R InterPro; IPR00446; HhH.

R Pfam; PF00730; HhH. GPD; 1.

R Pfam; PF00730; HhH. DI.

R Pfam; PF00730; HHH.; 1.

R Pfam; PF00633; HHH; 1.

R SMART; SM00478; ENDONUCLEASE_III_1; 1.

DR SMART; SM00525; FES; 1.

PROSITE; PS0154; ENDONUCLEASE_III_2; 1.

R PROSITE; PS0155; ENDONUCLEASE_III_2; 1.

R PROS
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Best Loc
Matches
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PIR; T43679; T43679.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIWKLANELV-DPVRPGDFNQALMELGAITCTPQSPRCSVCPISEICKAYQEQNVIRDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EL-----RGLPGLGPYTAAAVASIAFGERVAAVDGNVRRVLSRLFARESPKEKE---
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31.5%; Pred. No. 2.
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update) 3.2.2.-).

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RESULT 6
MUTY_BUCAI STANDARD;
ID MUTY_BUCAI STANDARD;
AC P57617;
DT 16-OCT-2001 (Rel. 40, Created)
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R InterPro; IPR004035; EndoIII_HhH.
InterPro; IPR004036; EndoIII_HhH.
R InterPro; IPR003651; FeS_bind.
R InterPro; IPR005760; MutY.
R InterPro; IPR005760; MutY.
R InterPro; IPR005760; MutY.
R Pfam; PF00633; HHH; J1.
R Pfam; PF00633; HHH; J1.
R SMART; SM00478; ENDO3c; 1.
R SMART; SM00525; FES; 1.
R SMART; SM00525; FES; 1.
R TIGRFAMs; TIGR01084; mutY; 1.
R PROSITE; PS01764; ENDONUCLEASE_III_1; 1.
R PROSITE; PS01755; ENDONUCLEASE_III_2; FALSE_NEG.
R PROSITE; PS01155; ENDONUCLEASE_III_2; FALSE_NEG.
R PROSITE; PS01155; ENDONUCLEASE_III_2; FALSE_NEG.
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Best Local S
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
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COFACTOR: Binds a 4Fe-4S cluster which is not important for the COFACTOR: Binds a 4Fe-4S cluster which is not important for the catalytic activity, but which is probably involved in the proper positioning of the enzyme along the DNA strand (By similarity).

SIMILARITY: BELONGS TO THE NTH/MUTY FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Adenine
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                                                                                                                                                                                                                                          QALMELGATVCLPKRPRCGACPLGAFCRGKEAPG--RYPAPRKRR
                                                                                                                                                                                                                                                                                                                      GAILSLSLDYFFPILEGNVKRILMRYYGIIGYVTEKKIEQKLWYLIELITPIH-NTGSFN
                                                                                                                                                                                                                                                                                                                                                                                AAVASIAFGERVAAVDGNVRRVLSRL-----FARESPKEKELFALAQGLLPEGVDPGVWN
                                                                                                                                                                                                                                                                                                                                                                                                                                       KALAAASLEEVLRVWQGAGYYRRAEHLHRLARSV-----EELPPSFAELRGLPGLGPYTA 114
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QSLNQSKLDDILCLWSGLGYYKRAENIYKTVKIIKEEFQEKPPTGFSDLIKLPGIGRSTA 122
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Pred. No. 2.7e-24;
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InterPro; IFR004035; EndoIII_FCL.
InterPro; IFR004036; EndoIII_HhH.
InterPro; IFR003651; FeS_bind.
InterPro; IFR003651; FeS_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shigenobu S., Watanabe H., Hattori M., Sakaki Y., "Genome sequence of the endocellular bacterial symbuchnera sp. APS.", Nature 407:81-86(2000).
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METAL
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PROSITE; PS00764; ENDONUCLEASE_III_2; 1.
PROSITE; PS001155; ENDONUCLEASE_III_2; 1.
DNA repair; Hydrolase; Glycosidase; Iron-sulfur;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Tokyo 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
Enterobacteriaceae; Buchno
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ATVCLPKRPRCGACPLGAFC---RGKEAPGRYPAPRKRRAKEERLVALVLLG---
                                   LNFFYPILDGNVKRILVRYYGISGLLKDKKIEKKLWNIIESITPIH-NTGKFNQGMMDIG
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Pred. No. 1.9e-22;
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                                                            -RESPKEKELFALAQGLLPEGVDPGVWNQALMELG
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PDB; 1KEA; 23-JAN-02
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InterPro; IPR004035; EndoIII_FCL,
InterPro; IPR004036; EndoIII_HhH.
InterPro; IPR003651; FeS_bind.
InterPro; IPR000445; HhH.
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                                                  PROSITE: PS00764; ENDONUCLEASE_III_1; 1.
PROSITE: PS00764; ENDONUCLEASE_III_2; 1.
DNA repair; Hydrolase; Glycosidase; Iron-sulfur;
Hypothetical protein; 3D-structure.
METAL 197 197 100-SULFUR (4FE-4S)
METAL 204 1RON-SULFUR (4FE-4S)
METAL 207 207 1RON-SULFUR (4FE-4S)
METAL 207 207 1RON-SULFUR (4FE-4S)
METAL 208 113 213 1RON-SULFUR (4FE-4S)
                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00730; HhH-GPD; 1. Pfam; PF00633; HHH; 1. SMART; SM00478; ENDO3c; 1. SMART; SM00525; FES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its working the proofit institutions as long as its content is in no way entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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NUCLELO ACIDS RES. 20:6501-6507(1992).

-!- FUNCTION: COULD ACT IN DNA REPAIR. RESTRICTION METHYLASE
M.MTHTI, WHICH IS ENCODED BY THIS PLASMID, GENERATES
CONDITIONS, SUBJECT TO DEAMINATION RESULTING IN G-T MISMATCHES.
CONDITIONS, SUBJECT TO DEAMINATION RESULTING IN G-T MISMATCHES.
-!- COPACTOR: BINDS A 4FE-48 CLUSTER WHICH IS NOT IMPORTANT FOR THE
CATALXTIC ACTIVITY, BUT WHICH IS PROBABLY INVOLVED IN THE PROPER
-!- SIMILARITY: BELONGS TO THE NTH/MUTY FAMILY.
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MEDLINB-93126090; PubMed-1336177;

Noelling J., van Eeden F.J.M., Eggen R.I.L., de Vos W.M.;

"Modular organization of related Archaeal plasmids encoding different restriction-modification systems in Methanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid pFV1.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
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01-APR-1993 (Rel. 25, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Possible G-T mismatches repair enzyme (EC 3.2.2.-) (ORF10).
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P29588;
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Query Match
Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
MUTY_AERHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DЬ
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                                                                                                                                          EMBL; X81473; -; NOT_ANNOTATED_CD;
HSSP; P17802; 1MUN.
InterPro; IPR003265; Endo_3c.
InterPro; IPR004035; EndoIII_FCL.
InterPro; IPR004035; EndoIII_Hhh.
                                                                            DNA repair; Hydrolase;
NON_TER 99 99
                                                                                              Pfam; PF00730; HhH-GPD; 1.

PROSITE; PS00764; ENDONUCLEASE_III_1; PARTIAL.

PROSITE; PS01155; ENDONUCLEASE_III_2; PARTIAL.
                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                            Jahagirdar R., Howard S.P.;
"ISOlation and characterization of a second exe operon required for Isolation and characterization of a second exe operon required for extracellular protein secretion in Aeromonas hydrophila.";
-I. FUNCTION: ADENINE GLYCOSYLASE ACTIVE ON G-A AND C-A MISPAIRS (BY SIMILARITY).

(BY SIMILARITY).
-I. COPACTOR: BINDS A 4FE-4S CLUSTER WHICH IS NOT IMPORTANT FOR THE POSITIONING OF THE ENZYME ALONG THE DNA STRAND (BY SIMILARITY).

-I. SIMILARITY: BELONGS TO THE NTH/MUTY FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95050248; PubMed=7961440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aeromonas hydrophila.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
A/G-specific adenine glycosylase (EC 3.2.2.-) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aeromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P46230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUTY_AERHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 TVCLPKRPRCGACPLGAFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 IICAPRKPKCEKCGMSKLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 LLAWYRENARPLPWRGEKDPYRVLVSEVLLQQTRVEQALPYYRRFLERFPTLKALAAASL
                                                                   99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGKKAAMVDANFVRVINRYFGGSYENLNYNHKALWELAETLVPGGKCRD-FNLGLMDFSA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGERVAAVDGNVRRVLSRLFARE----SPKEKELFALAQGLLPEGVDPGVMNQALMELGA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEVLRVWQGAGY-YRRAEHLHRLARSV-----EELPPSFAELRGLPGLGPYTAAAVASIA
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEIAKDIKEIGLSNORÄEQLKELARVVINDYGGRVPRNRKAILDLPGVGKYTCAAVMCLA 135
                                                                  ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                      NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aeromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                               11692 MW;
                      14.78;
51.78;
                                                                                        Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.1%;
31.7%;
                   Score 250.5;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gammaproteobacteria;
                                                       0806BDC67E1B0CB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 274.5; DB 1;
Pred. No. 1.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                    Iron-sulfur;
                .4e-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
                            DB 1;
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                                                                                    4Fe-4S
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                            Length
   Indels
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                              99;
1;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99287316; PubMed-10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.";

Nature 399:323-329(1999).
                                                                                                                                                                                                                                          use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                               This
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30-MAY-2000
16-OCT-2001
                                                                  Pfam;
                                                                                                                                                                                                                                                                                                              between
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STRAIN-MSB8 / DSM 3109;
MEDLINE-99287316; Pubme
                                         SMART;
                                                       Pfam;
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Bacteria; Thermotogae;
                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9WYK0;
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                                                                               InterPro;
                                                                                                                        InterPro;
                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endonuclease
                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: HAS BOTH AN APURLWIC AND/OR APYRIMIDINIC ENDACTIVITY AND A DNA N-GLYCOSYLASE ACTIVITY. INCISES DAY CYTOSINES, THYMINES AND GUANINES. ACTS ON A DAWAGED ST FROM THE DAWAGED SITE (BY SIMILARITY).

CATALYTIC ACTIVITY: The C-O-P bond 3, to the apurinic apyrimidinic site in DNA is broken by a beta-eliminatilleaving a 3, terminal unsaturated sugar and a product
                                                                                                                                                                                                                                                                                                                                                    COFACTOR: BINDS A 4FE-4S CLUSTER WHICH IS NOT IMPORTANT FOR THE CATALYTIC ACTIVITY, BUT WHICH IS PROBABLY INVOLVED IN THE PROPER POSITIONING OF THE ENZYME ALONG THE DNA STRAND (BY SIMILARITY). SIMILARITY: BELONGS TO THE NTH/MUTY FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                           leaving a 3'-terminal terminal 5'-phosphate.
                                                   rPro; IPR003265; Endo_3

rPro; IPR004035; EndoIII

rPro; IPR004036; EndoIII

rPro; IPR003651; FeS_bir

rPro; IPR003651; FeS_bir

rPro; IPR003583; HHH_1.

rPro; IPR003583; HHH_1.

rPro; IPR005759; Nth.

PF00730; HHH-GPD; 1.
                                                                                                                                                                           F72387; F72387; P20625; 2ABK.
                                                                                                                                                                                                     AE001716; AAD35453.1;
72387; F72387.
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               SM00525;
SM00278;
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(Rel.
(Rel.
                          ENDO3c; 1.
FES; 1.
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39,
40,
(EC
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, Last annotation updat
4.2.99.18) (DNA-(apur)
                                                                                             ннн_1.
                                                                                                                       FeS_bind.
                                                                                                                                   EndoIII_FCL.
EndoIII_HhH.
                                                                                                                                                                Endo_3c
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                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
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RESULT 10
UVEN_MICLU
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Best Local :
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Glycosidase;
METAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995
01-NOV-1997
28-FEB-2003
Ultraviolet
           EMBL;
                                            the European Bioinformatics Institute. There are no rest
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modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                 J. Biol. Chem. 270:23475-23484 (1995).

-I- FUNCTION: HAS BOTH, AN APRRINIC AND/OR APPRIMIDINIC INCLUSIVE AND A DNA N-GLYCOSYLASE ACTIVITY. INITIATES CIS-SYN PYRHMIDINE DIMERS. PROCEEDS VIA AN IMINO ENZINTERMEDIATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P46303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
METAL
                                                                                                           This
                                                                                                                                                                                                                                                          Piersen C.E., Prince M.A., Augustine M.L., Dodsc "purification and cloning of Micrococcus luteus endonuclease, an N-glycosylase/abasic lyase that
                                                                                                                                                                                                                                                                                                                                                           Micrococcus luteus (Micrococcus lysodeikticus).
Bacteria; Actinobacteria; Actinobacteridae; Act
Micrococcineae; Micrococcaceae; Micrococcus.
                                                                                                                                                                                                                                                                                                             STRAIN-ATCC 4698;
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00764; PROSITE; PS01155;
                                                                                                                                                                                                                                                 imino enzyme-DNA intermediate."
                                                                                                                                                                                                                                                                                                 MEDLINE=96007490; PubMed=7559510;
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1270
                                                                                                                                                                                                                                                                                                                                                                                                               glycosylase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UVEN_MICLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                    SIMILARITY: BELONGS TO THE NTH/MUTY FAMILY.
                                                                                                                                              CODONS FOR GLY-268
HAVE BEEN DETECTED.
                                                                                                                                                           MISCELLANEOUS: READTHROUGH OF T CODONS FOR GLY-268 AND ALA-270.
                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193
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                                    an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAFC---
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196
213
                                    email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 32, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
N-glycosylase/AP lyase (UV-endonu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
AAA86508.
2ABK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENDONUCLEASE_III_1;
ENDONUCLEASE_III_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 227; DB
Pred. No. 7.3e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                           OF 1-35
                                                                                                                                                             O. TWO
                                                                                                                                                                                                                                                                                                                                                                                                                           (UV-endonuclease) (Pyrimidine
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                                                                                                                                                             TERMINATOR
WO FORMS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₹
                                                                                                                                                                                                                                                                        Dodson M.L., Llo
uteus ultraviolet
                                                                                                                                                                                                                                                             that
                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 213;
                                                                                                                                                           UAG OCCURS
31 kDA AND
                                                                                                                                                                                                                                                             proceeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e proteome.
) (BY SIMILARITY).
) (BY SIMILARITY).
) (BY SIMILARITY).
) (BY SIMILARITY).
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                                                                                                                                                                                                 ENZYME: DNA
                                              y and fo
                                                                                                                                                                                                                                                                                    Lloyd
                                                     is
for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA repair;
                                                                                                                                                             32 kDA
                                                ch/announce/
                                                                                                                                                                                                             ΑŢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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CHAIN METAL METAL METAL METAL

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Query Match
Best Local S
Matches 70
                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                    RAUGA...
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
                                                                                                                                                                                                                                                                                                                                 NTHI_CAEEL STANDARD; PRT; 259 AA. P54137; Protection of the post of the post of the protection of the protection of the protection of the probable endonuclease III homolog (EC 4.2.99... probable endonuclease).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003265; Endo_3c.
InterPro; IPR004035; EndoIII_FCL.
InterPro; IPR004036; EndoIII_HhH.
InterPro; IPR003651; FeS_bind.
InterPro; IPR003645; HhH, 1.
InterPro; IPR0035759; Nth.
InterPro; IPR005759; Nth.
InterPro; IPR005759; Nth.
Pfam; PF00730; HhH-GPD; 1.
SMART; SM00478; ENDO3c; 1.
SMART; SM00478; ENDO3c; 1.
SMART; SM00278; HhH1; 1.
ISMART; SM00278; HhH1; 1.
FIGREAMS; TIGR01083; nth; 1.
PROSITE; PS01764; ENDONUCLEASE_III_1; 1.
PROSITE; PS01764; ENDONUCLEASE_III_1; 1.
PMOTOLASE: Nuclease: Endonuclease: Nua
                mitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
FUNCTION: Has both an apurinic and/or apyrimidinic endonuclease activity and a DNA N-glycosylase activity (By similarity).
apyrimidinic ACTIVITY: The C-O-p bond 3' to the apurinic or leaving a 3'-terminal unsaturated sugar and a product with a terminal 5'-phosphate.
COFACTOR: Binds a 4Fe-4S cluster which is not important for the catalytic activity, but which is probably involved in the proper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Nuclease; Endonuclease; Iron-sulfur; 4Fe-4S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 PSYAAGETDPERARALLAYELKPGREELLELLRAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 PYRVLVSEVLLQQT---RVEQALPYYRRFLERFPTLKALAAASLEEVLRVWQGAGYYR-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----RGKEAPGRYPAPRKRRAK--EERLVALVLLGR 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRLGETDETDPGKGR-ARRGRPVPPARDWTMLSHRLIFHGRRVCHARRPACGRCPIARWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRL-FARESPKEKELFALAOGLLPEGVDPGVWNOALMELGATVCLPKRPRCGACPLGAFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFELLVATVĽSAQTTDVKVNAATP----ALFARFPDAHÁMAÁÁTEPELQELVRSTGFYRNK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASAILRLSQELVGRHDGEVPARLEDLVALPGVGRKTAFVVLGNAFGQPGITVDTHFGRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEHLHRLARSV-----EELPPSFAELRGLPGLGPYTAAAVASIAFGERVAAVDGNVRRVL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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279
203
210
213
213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 199;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRON-SULFUR (4FE-4S) (BY SIMILARITY)
IRON-SULFUR (4FE-4S) (BY SIMILARITY)
IRON-SULFUR (4FE-4S) (BY SIMILARITY)
IRON-SULFUR (4FE-4S) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UV ENDONUCLEASE 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C385369A1827C005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA repair; Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; 1
.5e-08;
es 95;
                                                                                                                                                                                                                                                                                                                                                      .18)
                                                                                                                                                                                                                                                                                                                                               (DNA-(Apurinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kDa
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                RESULT
END3_BA
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                                                                                                                          739788;
01-FEB-1995 (Rel. 31, Created
01-FEB-1995 (Rel. 31, Last se
28-FEB-2003 (Rel. 41, Last ar
3 Probable endonuclease III (Ev
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Best Local S
Matches 58
   MEDLINE-95219085;
                                                                                   Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                 LT 12
_BACSU
                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R WORMPEP: R108.5; CE03559.

R InterPro; IPR003255; Endo_3c.

R InterPro; IPR004035; EndoIII_HCL.

InterPro; IPR004035; EndoIII_HHH.

InterPro; IPR004036; EndoIII_HHH.

InterPro; IPR00445; HhH.

InterPro; IPR00445; HhH.

InterPro; IPR00445; HhH.

InterPro; IPR000445; HhH.

InterPro; IPR00045; INTERPORTE; PR00730; HHH-GP; 1

Pfam; PF00730; HHH-GP; 1

Pfam; PF00730; HHH-GP; 1

SMART; SM00478; ENDO3C; 1

SMART; SM00478; ENDONUCLEASE_III_1; 1.

PROSITE; PS00764; ENDONUCLEASE_III_2; 1.
                                                                                                                                                                                                                                             END3_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METAL
METAL
METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP;
                                                                                                                                                                                                                                                                                                                                 200
                                                                                                                                                                                                                                                                                                                                                                197
                                                                                                                                                                                                                                                                                                                                                                                     141 -FARESPKEKELFALAQGLLPEGVDPGVW----NQALMELGATVCLPKRPRCGACPLGAFC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 YRVLVSEVLLQOTRVEQALÞYYRRFLERFFTLKALAAASLEEVLRVWOGAGYY-RRAEHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 250874; CAA90766.1; -. T24131; T24131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bloinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POSITIONING OF THE ENZYME along the DNA strand (By similarity).
SIMILARITY: BELONGS TO THE NTH/MOTY FAMILY.
                                                                                                                                                                                                                                                                                                                             R 200
                                                                                                                                                                                                                                                                                                                                                            R 197
                                                                                                                                                                                                                                                                                                                                                                   GWIKTSTPEKTQKAL-EILLPK----SEWQPINHLLVGFGQMQCQPVRPKCGTC----LC
                                                                                                                                                                                                                                                                                                                                                                                                                                   QKTAKILKDDFSGDIPDSLDGLCALPGVGPKMANLVMQIAWGECVGIAVDTHVHRISNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HRLARSVE-----ELPPSFAELRGLPGLGPYTAAAVASIAFGERVA-AVDGNVRRVLSRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FQVLVALMLSSOTRDEVNAAAMKRLKDHGLSIGKILEFKVPDLETILCPVGFYKRKAVYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203
259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
PubMed=7704260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187
194
197
                                                                                Bacillales;
                                                                                                                                     Last sequence update)
Last annotation update)
III (EC 4.2.99.18) (DNA-(apurinic
                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28841 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /drolase; Nuclease; Endonuclease;
DNA repair; Glycosidase; Lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 176; DB 1;
Pred. No. 8.8e-07;
3; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRON-SULFUR (4FE-4S) (BY SIMILARITY).
IRON-SULFUR (4FE-4S) (BY SIMILARITY).
IRON-SULFUR (4FE-4S) (BY SIMILARITY).
IRON-SULFUR (4FE-4S) (BY SIMILARITY).
F52E57810571EDBC CRC64;
                                                                          Bacillaceae;
                                                                                                                                                                                                                                219
                                                                                                                                                                                                                                AA
                                                                        Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Iron-sulfur;

20;

8

140 88

148

δ В δ DЬ δ 8 õ

161

CAEEL

RESULT
NTHLCAN
ID HOTO
ID TO 10
ID TO 1

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RA Kunst F. Ogasawara N. Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Bourschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Entlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Glispepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Guiseppi G., Guy B.J., Haga K., Klain G., Krogh S., Kumano M.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kunita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Medina N., Mellado R.P., Nizumo M., Moesti D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi M., Tamakoshi A., Tanaka T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RT Withis S., Vandenbol M., Vannier F., Vata K.,
Toghida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
The Complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                 EMBL; U11289; AAA80005.1; -.
EMBL; L47709; AAB38457.1; -.
EMBL; Z99115; CAB14150.1; -.
PIR; 140525; I40525.
HSSP; P20625; 2ABK.
Subtilist; BG10956; nth
                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                              entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence analysis of the Bacillus subtilis chromosome region between the serA and kdg loci cloned in a yeast artificial chromosome."; Microbiology 142:2005-2016(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serror P
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MEDLINE=96349105; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bruand C., Sorokin A., Serror P., Ehrlich S.D "Nucleotide sequence of the Bacillus subtilis Microbiology 141:321-322(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 300:249-256(1997).

Acture 300:249-256(1997).

Acture 300:249-256(1997).

Acture 300:249-256(1997).

Acture 300:249-256(1997).

Apyrimidinic site in DNA is broken by a beta-elimital apyrimidinic site in DNA is broken by a beta-elimital apyrimidinal solution in Section 1 approximate approximate solution approximate solution approximate solution approximately.

Acture 300:249-256(1997).

Acture 300:249-256(1997).

Acture 300:249-256(1997).

Approximately 100:249-256(1997).

Acture 300:249-256(1997).

Acture 300:249-256(1997
                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.V., Azevedo
   IPR003265;
IPR004035;
IPR004036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed-8760912;
vedo V., Zumstein
Endo_3c.
EndoIII_FCL.
EndoIII_HhH.
                                                                                                                                                                                                                                                                                                                                                                                  institutions as long as
                                                                                                                                                                                                                                                                                                                        moved. Usage by and fo
(See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d 3' to the apurinic or
n by a beta-elimination
sugar and a product wit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Galleron
                                                                                                                                                                                                                                                                                                                                                    Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOT IMPORTANT FOR THE INVOLVED IN THE PROPERTRAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                               its content
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for
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ID Y613_METJA
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Best Local S
Matches 56
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RE InterPro; IPR005759; Nth.

RE Pfam; PF00730; RhH-GPD; 1.

RE Pfam; PF00633; HHH; 1.

RE SMART; SM00478; ENDO3C; 1.

RE SMART; SM00478; ENDO3C; 1.

RE SMART; SM00525; FES; 1.

RE SMART; SM00578; HhH;; 1.

RE TIGRPAMS; TIGR01083; nth; 1.

RE PROSITE; PS00764; ENDONUCLEASE_III_2; 1.

RE PROSITE; PS01155; ENDONUCLEASE_III_2; 1.

RETGRPAMS; TIGN-SULFUR (4FE-4S) (BY SIMILARI INTERIOR (4F
                                                                                                                                         STRAIN-LAL-1 / DSM 2661 / ATCC 43067;
STRAIN-LAL-1 / DSM 2661 / ATCC 43067;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Putative endonuclease MJ0613.
                                                                             Science 273:1058-1073(1996).
-!- SIMILARITY: BELONGS TO THE NTH/MUTY FAMILY.
                                                                                                                                 "Complete genome jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methanococcus jannaschii
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56; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HCKAQSPRCAECPLLSLCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YRNKAKNIQKLSKMIIEDYGGEVPRDRDELVKLPGVGRKTANVVVSVAFGVPAIAVDTHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YR-RAEHLHRLARSV-----EELPPSFAELRGLPGLGPYTAAAVASIAFGERVAAVDGNV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPYRVLVSEVLLQQ-----TRVEQALPYYRRFLERFPTLKALAAASLEEVLRVWQGAGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERVSKRLGICRWKDSVLEVEKTLMRKVPKE---
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Pred. No. 1.5e
30; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344
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.5e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187
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Best Local S
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R InterPro; IPRO03265; Endo_3c.
R InterPro; IPRO04035; EndoIII_HhH.
R InterPro; IPRO04035; EndoIII_HhH.
R InterPro; IPRO03583; HHH.
R Pfam; PP01986; DUF123; 1.
R Pfam; PP00730; HhH-GpD; 1
R Pfam; PP00730; HHH-GPD; 1
R Pfam; PP00633; HHH; 1.
R ProDom; PD01467; DUF123; 1.
R PSMART; SM00478; ENDO3C; 1.
R SMART; SM00478; ENDO3C; 1.
R SMART; SM00525; FES; 1.
R SMART; SM00278; HhH1; 1.
R SMART; SM00278; HH11; 1.
R SMART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY. MEDLINE-97144402; Pubmed-8990169; Aspinwall R., Rothwell D.G., Roldan-Arjona T., Anselm
                                                                                                                                                    NTH1.HUMAN STANDARD; PRT; 312 AA. P78549; 099566; 099794; 099Byz; 312 AA. 28 FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Endonuclease III-like protein 1 (EC 4.2.99.18).
                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                      _HUMAN
                                                                                               NCBI_TaxID=9606;
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METAL
METAL
METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial or send an email to license egreement (See http://www.isb-sib.ch/announce/
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55; Conser
                                                                                                                                                                                                                                                                                                                                                                                      REICSSK-SKCDKC
                                                                                                                                                                                                                                                                                                                                                                                                                            ATVCLPKRPRCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGERVAAVDGNVRRVLSR--LFARESPKEKELFALAQGLLPEGVDPGVW----NQALMELG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKLADLIY PÄĞFYKNKAKNLKKLAKILKENYNGKV PDSLEELLKL PG VGRKTANLVITLA
                                                                                                                                                                                                                                                                                                                                                                                                                                             FNKDGICVDTHVHRICNRWEIVDTETPEETE-FELRKKLPKK-----YWKVINNLLVVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEVLRVWOGAGYYR-RAEHLHRLARSVEE-----LPPSFAELRGLPGLGPYTAAAVASIA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLKKLNKNAVVTEIAKDKDPFKVLISTIISARTKDEVTEEVSKKLFKEIKDVDDLLNIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLAWYRENARPLPWRGEKDPYRVLVSEVLLQQTRVEQALPYYRRFLERFPTLKALAAASL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteome.
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190
193
201
344 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; Hydrolase; Glycosidase; Iron-sulfur; 4Fe-4S;
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190
193
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28.4%;
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                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Pred. No. 3e-06;
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IRON-SULFUR (4FE-4S) (BY SIMILARITY).
IRON-SULFUR (4FE-4S) (BY SIMILARITY).
IRON-SULFUR (4FE-4S) (BY SIMILARITY).
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  Anselmino
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  c.,
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RX MEDITNE-22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schammen C.M., Schuler G.D.,
RA Altschil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helleh F.,
RA Billeton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fishey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Finnan and mouse cDNA sequences ",
RC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                   MEDITINE-97107855; PubMed-9045706; Hilbert T.P., Chaung W., Boorstein R.J., Cunningham R.P., Teebor "Cloning and expression of the cDNA encoding the human homologue the DNA repair enzyme, Escherichia coli endonuclease III."; J. Biol. Chem. 272:6733-6740(1997).
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 8-312 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE-9837098; PubMed-9705289; Ikeda S., Biswas T., Roy R., Izumi T., Boldogh I., Kurosk. Sarker A.H., Seki S., Mitra S.; "Purification and characterization of human NTH1, a homolescherichia coli endonuclease III. Direct identification the active nucleophilic residue."; J. Biol. Chem. 273:21585-21593(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 7-312 FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 6-312 FROM N.A., FUNCTION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rieder M.J., Braun A.C., Montoya M.A., Chung M.-W., Nguyen C. Nguyen D.A., Livingston R.J., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A., Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ricke D.O., Bruce D., Mundt M., Doggett N., Munk C., Robinson D., Jones M., Buckingham J., Chasteen L., T Goodwin L., Bryant J., Tesmer J., Meincke L., Longmi Ueng S., Tatum O., Campbell C., Fawcett J., Maltbie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genomic structure and sequence Escherichia coli endonuclease II TSC2 and SLC9A3R2 genes.", Gene 222:287-295(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99051340; PubMed-9831664; Imai K., Sarker A.H., Akiyama K., Shohmori T., Seki S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and characterization of a functional human Escherichia coli endonuclease III."; Proc. Natl. Acad. Sci. U.S.A. 94:109-114(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ward C.J., Ch
Hickson I.D.;
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(SEP-1998) to the EMBL/GenBank/D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.A.
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O02) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND FUNCTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ce of a human homologue (NTHL1/NTH1) c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ikeda S., Yao
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fication of
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ire J., White
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Lys-212
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"Cell-cycle regulation, intracellular sorting and induced overexpression of the human NTH1 DNA glycosylase involved of formamidopyrimidine residues from DNA.";
Mutat. Res. 460:95-104(2000).
                                                                                        IIM; 602566; .

OG: 600.005644; C:nucleus; IDA.

OG: 600.0019104; F:DNA N-glycosylase activity; ID

GO: GO: 0004519; F:endonuclease activity; TAS.

GO: GO: 0004519; F:endonuclease activity; TAS.

GO: GO: 0006296; P:nucleotide-excision repair; TAS.

GO: GO: 0006296; P:nucleotide-excision repair, DN

InterPro; IPR003265; Endo_3c.

InterPro; IPR0040365; EndoIII_HhH.

InterPro; IPR00403651; FeS_bind.

InterPro; IPR000445; HhH.

InterPro; IPR000445; HhH.
                                                                                                                                                                         -I- FUNCTION: Has both an apurinic and/or apyrimidinic endonuclease activity and a DNA N-glycosylase activity. Incises damaged DNA at cytosines, thymines and guanines. Acts on a damaged strand, 5' from the damaged site. Regulired for the repair of both oxidative DNA damage and spontaneous mutagenic lesions.
-I- CARALYTIC ACTIVITY: The C-O-P bond 3' to the appurinic or apyrimidinic site in DNA is broken by a beta-elimination reaction, leaving a 3'-terminal unsaturated sugar and a product with a terminal 5'-phosphate.
-I- COFACTOR: Binds a 4Fe-4S cluster which is not important for the catalytic activity, but which is probably involved in the proper positioning of the enzyme along the DNA strand.
-I- SIBCELLULAR LOCATION: Nuclear.
-I- TISSUE SPECIFICITY: Widely expressed with highest levels in heart and lowest levels in lung and liver.
-I- DEVELOPMENTAL STAGE: Expression levels are regulated during the call cycle with increased levels during early and mid S-
                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
             SMART; SM00478; ENDO3C; 1.
SMART; SM00525; FES; 1.
PROSITE; PS00764; ENDONUCLEASE_III_1;
PROSITE; PS01155; ENDONUCLEASE_III_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ikeda S., Kohmoto T., Tabata R., Seki Y.;
"Differential intracellular localization of the endonuclease III homologs and analysis of the so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22419222; PubMed=12531031; Ikeda S., Kohmoto T., Tabata R., S
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SEQUENCE OF 9-312 FR
DEVELOPMENTAL STAGE.
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SIMILARITY:
CAUTION: It
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L; AB014460; BAA32695.1; ALT_INIT.
L; AC005600; AAC34209.1; ...
L; AF498098; AAM11786.1; ...
L; AB001575; BAA19413.1; ALT_INIT.
L; U81285; AAC51136.1; ALT_INIT.
L; BC003014; AAH03014.1; ALT_INIT.
L; BC003014; AAH03014.1; ALT_INIT.
L; BC003014; AAH03014.1; ALT_INIT.
L; Y09687; CAA70865.1; ...
EW; HGNC.8028; NTHL1.
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   Nuclease;
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ннн; 1.
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   Endonuclease;
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Multifunctional enzyme;
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                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., FUNCTION, AND TISSUE SP. STRAIN-BALB/C;
MEDLINE-98417643; PubMed-9743625;
Sarker A.H., Ikeda S., Nakano H., Terato H. Akiyama K., Tsutsui K., Bo Z., Kubo K., Yam. Yoshida M.C., Seki S.;
"Cloning and characterization of a mouse home and the coll endonuclease III.";
J. Mol. Biol. 282:761-774(1998).
                                                                                                                                                                                                                             homologue
Submitted
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SEQUENCE FROM N.A.

STRAIN-C5784683; TISSUE-Cecum;

MEDLINE-22354683; PubMed-12466851;

Okazaki Y., Furuno M., Kasukawa T., Adachi J.,

Okazaki O., Osato N., Saito R., Suzuki H., Yasukawa Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Subaldarelli R., Hill D.P., Bult C., Hume D.A.,
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035980;
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ACT_SITE
                                                                                                                                                                                                                       "Complete genomic DNA sequence homologue 1 gene (NTH1)."; submitted (SEP-1997) to the EM
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28-FEB-2003 (Rel. 41,
28-FEB-2003 (Rel. 41,
Endonuclease III-like
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Bjoras M.,
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protein 1 (EC 4.2.99.18).
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K->Q: INACTIVATES ENZYME.
K->R: 85-FOLD REDUCTION IN
MT -> TS (IN REF. 8).
MISSING (IN REF. 8).
M -> I (IN REF. 1).
T -> A (IN REF. 1).
T -> A (IN REF. 1).
                                                                                                                                                                                                                             EMBL/GenBank/DDBJ
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Pred. No. 8.6e-06;
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Sciurognathi; Muridae,
                                                                                                                                                                                                                                                                              Hoff E.
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Schonbach C.
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R EMBL; AB006812; BAA22080.1;
R EMBL; AB009371; BAA28846.1;
R EMBL; A9001517; CAB65239.1;
R EMBL; Y09688; CAA70866.1;
R EMBL; Y09688; CAA70866.1;
R EMBL; AK033701; BAC28435.1; ALT_FRAME.
R GO; GO:0005739; C:mitochondrion; IDA.
R GO; GO:0005739; C:mitochondrion; IDA.
R GO; GO:0019104; F:DNA N-glycosylase activity; IDA.
R GO; GO:0019104; F:DNA N-glycosylase activity; IDA.
R GO; GO:006296; P:nucleotide-excision repair, DNA incision, 5.
R InterPro: IPR004036; EndO_3C.
R InterPro: IPR004036; EndO_3II. HhH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RY SUBCELLULAR LOCATION.

RY SUBCELLULAR LOCATION.

RX MEDLINE-2241922; PubMed-12531031;

RA Ikeda S., Kohmoto T., Tabata R., Seki Y.;

RT This ferential intracellular localization of the human and mouse for the sorting signals.";

RT This ferential intracellular localization of the sorting signals.";

RT This ferential intracellular localization of the sorting signals.";

RT This ferential intracellular localization of the sorting signals.";

RT THOMATON: Has both an apurinic and/or apprimidinic endonuclease crivity and a DNA N-glycosylase activity. Incises damaged DNA at CC cytosines, thymines and guanines. Acts on a damaged strand, 5' CC from the damaged stre. Required for the repair of both oxidative activity. The C-O-p bond 3' to the apurinic or leaving a 3'-terminal unsaturated sugar and a product with a cc leaving a 3'-terminal unsaturated sugar and a product with a cc catalytic activity, but which is probably involved in the proper cc similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Frazer K.S., RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., RA Konajaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., RA Konajaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Sultana R., Wayner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., RA Wilming L.G., Wynshaw-Borls A., Yanagisawa M., Yang I., Yang L., Yang L., Zavolan M., Zhu Y., Zimmer M., Carninci P., Hayatsu N., RA Hara A., Hashizume W., Imotani K., Ishii y., Itoh M., Kagawa I., RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., RA Hara A., Hashizume W., Sasaki D., Shibata K., Shinagawa A., RA Birney E., Hayashizaki Y., Sasaki D., Shibata K., Shinagawa A., Ra Birney E., Hayashizaki Y., Sasaki D., Shibata K., Shinagawa A., Ra Birney E., Hayashizaki Y., Sasaki D., Shibata K., Shinagawa A., Ra Birney E., Hayashizaki Y., Sasaki D., Shibata K., Shinagawa A., Ra Birney E., Hayashizaki Y., Sasaki D., Shibata K., Shinagawa A., Ra Birney E., Hayashizaki Y., Sasaki D., Shibata K., Shinagawa A., Ra Birney E., Hayashizaki Y., Sasaki D., Shibata K., Shinagawa A., Ra Birney E., Hayashizaki Y., Sasaki D., Shibata K., Shinagawa A., Shinagawa S., Sh
                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee@ibb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Mitochondrial.
TISSUE SPECIFICITY: Widely expressed.
SIMILARITY: BELONGS TO THE NTH/MUTY FAMILY.
CAUTION: Ref. 3 sequence differs from that shown due frameshift in position 33.
           EndoIII_HhH
FeS_bind.
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PROSITE; PS00155; ENDONUCLEASE_III_2; 1.

WHYDROLAGE; Nuclease; Endonuclease; Multifunctional enzyme; DNA repair; WGlycosidase; Lyase; Iron-sulfur; 4Fe-45; Mitochondrion.

PT ACT_SITE 208 208 NUCLEOPHILE IN THE N-GLYCOSYLASE REACTION (BY SIMILARITY).

PT METAL 278 REACTION (BY SIMILARITY).

PT METAL 285 285 IRON-SULFUR (4FE-4S) (BY SIMILARITY).

PT METAL 286 286 IRON-SULFUR (4FE-4S) (BY SIMILARITY).

PT METAL 287 298 IRON-SULFUR (4FE-4S) (BY SIMILARITY).

PT METAL 298 298 IRON-SULFUR (4FE-4S) (BY SIMILARITY).

PT CONFLICT 112 112 P-> S (IN REF. 3).

SQ SEQUENCE 300 AA; 33646 MW; A7D771FFD7BC1939 CRC64;
                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                      Query Match
Best Local :
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             258
                                         163
                                                      200 VALPGVGPKMAHLAMAVAWGTISGIAVDTHVHRIANRL--RWTKKMTKTPEETRKNLEEW
                                                                                                                                140
                                                                                                   104
                                                                                                                                                              50
                                                                                                                                                                                            80
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                                                                                                                                                                                                                                                       56,
LPRVLWSEVNGLLVGFGQQICLPVHPRCQACLNKALC
                             VDPGVW----NQALMELGATVCLPKRPRCGACPLGAFC
                                                                                                                                                                                                                                                Similarity 25.8
56; Conservative
                                                                                RGLPGLGPYTAAAVASIAFGE-RVAAVDGNVRRVLSRLFARESPKEKELFALAQGLLPEG
                                                                                                              QRLRARGLTVESILQTDDDTLGRLIYPVGFWRNKVKYIKQTTAILQQRYEGDIPASVAEL
                                                                                                                                          RRFLERFPTLKALAAASLEEVLRVWQGAGYYR-RAEHLHRLARSVE-----ELPPSFAEL 103
                                                                                                                                                                         WQQQLANIRIMRSKKDAPVDQLGAEHCYDASAPPKVRRYQVLLSLMLSSQTKDQVTAGAM 139
                                                                                                                                                                                                      WYRENARPLPWRGEKDP-----49
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                                                                                                                                                                                                                                               41; Mismatches
                                                                                                                                                                                                                                                               Pred
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Multifunctional enzyme; DNA repair;
                                                                                                                                                                                                                                             1.4e-05;
ches 87;
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 294
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Search completed: September 15, 2003, 13:51:14 Job time : 25 secs

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Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-09-107-532A-7308
US-09-813-574-2
US-09-813-574-9
US-09-198-452A-421
US-09-198-452A-421
US-09-650-855-37
US-09-650-855-37
US-09-650-855-37
US-09-134-001C-4684
US-09-134-001C-4684
US-09-107-532A-3843
US-08-808-550-39
US-08-808-550-39
US-08-808-550-37
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Result

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6.2	6.2	6.2	6.3	6.4	6.4	6.4	6.5	6.5	6.6	6.7	6.8	6. 8	6.8	6.9	7.0	7.1	7.5
657	798	435	427	460	1580	1580	1729	675	316	425	702	542	494	230	776	4472	212
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US-09-252-991A-28001	US-09-252-991A-25309	US-09-252-991A-24914	US-09-252-991A-30434	US-09-328-352-4274	US-08-804-198-5	US-08-804-227C-11	US-09-553-690-2	US-09-252-991A-29650	US-09-252-991A-30325	US-09-252-991A-26326	US-09-252-991A-31609	US-09-252-991A-21753	US-09-252-991A-17295	US-09-328-352-5770	US-09-252-991A-28446	US-08-804-227C-2	US-09-252-991A-17572
Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	.Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence
28001, A	25309, A	24914, A	30434, A	4274, Ap	5, Appli	11, Appl	2, Appli	29650, A	30325, A	26326, A	31609, A	21753, A	17295, A	5770, Ap	28446, A	2, Appli	17572, A

ALIGNMENTS

RESULT 1

US-09-107-532A-7308

; Sequence 7308, Application US/09107532A

; Patent No. 6583275

; GENERAL INFORMATION:
 APPLICANT: Lynn A Doucette-Stamm an TITLE OF INVENTION: NUCLEIC ACID ANT ENTEROCOCCUS FAI NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...4
SEQUENCE DESCRIPTION: SEQ ID NO: US-09-107-532A-7308 INFORMATION FOR SEQ ID NO: 7308: SEQUENCE CHARACTERISTICS: LENGTH: 403 amino acids APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES TELECOMMUNICATION INFORMATION: TELEPHONE: (781)893-5007 COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660 CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION FEATURE: ORIGINAL SOURCE: CURRENT APPLICATION DATA: NUMBER OF SEQUENCES: 7310 CITY: Waltham STATE: Massachusetts ORGANISM: Enterococcus faecium OPERATING SYSTEM: <Unknown> COMPUTER: SOFTWARE: ASCII TELEFAX: (781)893-8277 STREET: 100 Beaver Street (B) LOCATION 1...403 and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

Query Match Best Local Similarity

118;

32

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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/013,13
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08813574 Patent No. 6013473 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version
APPLICATION NUMBER: US/08/813,574
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330 QTRHLGEVTHIFSHLKWHVLLFYGRATEGAEQEFTENKTSKWLKPDAFDSVVFPKVQMKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 RSRPLGEVRHALTHRRLRVEV-RGALWEGEGED------PWKRP-----LPKLMEKV 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270 RDSQKLLANMWTFPMMEVTQEEYERLKKEWETKPEIDLFDDLVAEEEGONLPFEKQELFVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 CLPKRPRCGACPLGAFC----RGKEAPGRYPA-PRKRRAKEERLVALVLLGRKGVH---- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 CTPTSPKCETCPIQAFCLANKRGIQT--SFPVKTKKAKPKDVYYISAALQNHSGAYYFEE 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 LPEPAVDGNVMRVVSRLECIEADIAKASSRKIFDEAMRKIIDEKHPGEENQAMMDLGSAI 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 ERVAAVDGNVRRVLSRLFARES----PKEKELFALAQGLLPEGVDPGVWNQALMELGATV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 KLLKAWEGLGYYSRARNIQAAAKQIMSEFDGEMPQTPEEISSLKGIGPYTTGAIASIAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVLRVWQGAGYYRRAEHLHRLARSV-----EELPPSFAELRGLPGLGPYTAAAVASIAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IOWY EQEKRNÍ PWRYNRDPYRIWI SEIMLOOTRVDTVI DYFYRFMEWFPTI EELANA PEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dlarity 29.7%; Score 505; DB 4; L 23.7%; Pred. No. 1.4e-42; Conservative 66; Mismatches 113;
                                                                                                                                                                                                                                                                                 60/013,132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91
                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/0704,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NO 33310
TYDE: DATE: 1998-07-27
SEQ ID NO 33310
TYDE: DATE: 1998-07-27
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US-09-252-991A-23310
; Sequence 23310, Appl
; Patent No. 6551795
; Patent No. 6551795
                                                                                                                                                                                                                                                 i LENGTH: 470
TYPE: PRT
CORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23310
                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                 Matches
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TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-813-574-2
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Matches 136; Conserv
116 AVASIAFGERVAAVDGNVRRVLSRLFARE----SPK-EKELFALAQGLLPEGVDPGVWNQ
                                                                                              119 EGFNGAVLDWYDRHGRKDLPWQQGITPYRVWVSEIMLQQTQVSTVLGYFDRFMAALPDVE 178
                                                              61 ALAAASLEEVLRVWQGAGYYRRAEHLHRLA-----RSVEELPPSFAELRGLPGLGPYTAA 115
                                                                                                                                                                                              126;
                                                                                                                    2 EAWRKALLAWY-RENARPLPWRGEKDPYRVLVSEVLLQQTRVEQALPYYRRFLERFPTLK 60 | : |:| | : | : | : | : | : | : |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          378 RPNSGLLAGIWEFPSVTWEPSEQLORKALLQELQRWAGPLPATHLRHLGEVVHTFSHIKL 437
                                 ALAAAAEDEVLHLWTGLGYYSRARNLHKTAQIVVERHAGEFPRDVEQLAELPGIGRSTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 R-LEGREQGLYGVP--LEPPEELPGREAAF------GVRSRPLGEVRHALTHRRL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318 CAPNTGOCHLCLPPSEPWDOTLGVVNFPRKASRKPPREESSATCVLEQPGALGAQILLVO 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 -AP-----LGRKGVHLE 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 PARPGDENQAAMELGATVCTPQRPLCSQCPVESLCRARQRVEQEQLLASGSLSGSPDVEE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 GVDPGVWNQALMELGATVCLPKRPRCGACPLGAFCRGKE------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 MQKWPTLQDLASASLEEVNQLWAGLGYYSRGRRLQEGARKVVEELGGHMPRTAETLQQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 LERFPTLKALAAASLEEVLRVWQGAGYYRRAEHLHRLARS-VEEL---PPSFAEL--RGL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 VTAFRGSLLSWYDQEKRDLPWRRRAEDEMDLDRRAYAVWVSEVMLQQTQVATVINYYTGW 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VEAWRKALLAWYRENARPLPWRG------EKDPYRVLVSEVLLQQTRVEQALPYYRRF 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVEVRGALWEGE 290
                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09252991A
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                                                                                                                                                                         28.1%; Score 477.5; DB 4; Length 470; 36.2%; Pred. No. 1.1e-39; tive 58; Mismatches 119; Indels 45
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                                                                                                                                                                       Indels 45;
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                                   238
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RESULT 2 US-08-813-574-2

APPLICANT: Wei, Ying TITLE OF INVENTION: NUMBER OF SEQUENCES:

Ying-Fei

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett

Diskette

COUNTRY: UZIP: 19406

USA

STREET: 709 SwedeLand CITY: King of Prussia STATE: PA

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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 535 amino acids

TELEFAX:

610-270-4026

TYPE:

amino acid

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NUMBER OF SEQ ID NOS: 6
SEQ ID NO 421
LENGTH: 375
TYPE: PRT
ORGANISM: Chlamydla pn
US-09-198-452a-421
                                                                                                                                                                                               US-08-813-574-9
                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-09-198-452A-421
                                                                                                                                 Sequence 9, Application Patent No. 6013473 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION: APPLICANT: Griffais,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/198,452A CURRENT FILING DATE: 1998-11-24 NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve TITLE OF INVENTION: and treatment of infection FILE REFERENCE: 9710-003-999
                                                                          APPLICANT: Wei, Ying-Fei
TITLE OF INVENTION: Human
NUMBER OF SEQUENCES: 18
                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                           320 VHL 322
                                                                                                                                                                                                                                                                                                                                                           260
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                                                                                                                                                                                                                                                                                                                                                       KRRPKEMMAGLYEFPYIEVEPEEGLQDIEGFTKKMELSLESPLEFLGNLKEQRHAFTNHK
                                                                                                                                                                                                                                                                                                                                                                                              LERLEGREQGLYGVPLFPPEELPGREAAFGVRSR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                   GACIC-KKVPQCHRCPVRQACGAWRENKQFVLPVRHARKKVIFLHRLVAIVLYDGSLVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATVCLPKRPRCGACPLGAFCRGKEAPGRYPAPRKRRAKE----ERLVALVLL-GRKGVH 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFKRRAAAVDGNVLRVLSRIFLIETSIDLESTRTWVSRIAQALLPH-KSPEVIAEALIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFGERVAAVDGNVRRVLSRLFARESPKEKE-----LFALAQGLLPEGVDPGVWNQALMEL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEEDVIKLWEGLGYYSRARHLLEGARMVMEEFHGKIPDDAISLAQIRGVGPYTVHAILAF 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLEEVLRVWQGAGYYRRAEHLHRLARSVEE-----LPPSFAELRGLPGLGPYTAAAVASI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EALKKWFEKNKRSLPWRDNPTPYSVWVSEVMLQQTRAEVVIDYFNQWMERFPTIESLAAA
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                                                                                              Human Muty
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                                                                                                                                                                                           RESULT 6
US-09-651-656-37
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MOLECULE TYPE: protein US-08-813-574-9
Patent NO. VITUE
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MCCUTHEN-MALONEY, SANDRA
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
APPLICANT: LAWRENCE LIVERMORE NATIONAL PROBLEM NATIONS, DIA MUT.
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                                                                                                                                                    Sequence 37, Application US/09651656 Patent No. 6340566
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/0 FILING DATE: 11-MAR-1996 ATTORNEY/AGENT INFORMATION: NAME: Han, William T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: AT TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SmithKline
STREET: 709 Swedeland
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 610-270-4026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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                                                                                                                                                                                                                                                                     PVSSFTGCMDEGNALWYNLAQPPSVGLAAPVERLLQQ-LRTGAPV
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linear
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35.1%;
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Pred. No. 2.8e-39;
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                                                       DNA MUTATIONS
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; ORGANISM: Escherichia
US-09-650-855-37
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TITLE OF INVENTION: MUTATIONS, DNA SEQUENC
FILE REFERENCE: IL-10284
CURRENT APPLICATION NUMBER: US/09/650,855
CURRENT ELLING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: 05/192,764
PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-650-855-37
                                                                                                                                                                                                                                              SOFTWARE:
SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37, Application US/09650855
Patent No. 6365355
GENERAL INFORMATION:
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: TYPE: PRT
: ORGANISM: Escherichia coli
US-09-651-656-37
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MCGUTHEN-MALONEY, SANDRA
APPLICANT: LAWRENCE LIVERNORE NATIONAL LABORATORY
TITLE OF INVENTION: CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA
TITLE OF INVENTION: MUTATIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND DNA
                                                                                                                                                                                                               TYPE: PRT
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Best Local
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CURRENT FILING DATE: 2000-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: FILE REFERENCE: IL-
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                       10 VLDWYDKYGRKTLPWOIDKTPYKVWLSEVNLOOTQVATVIPYFERFMARFPTVTDLANAP
                                    8 LLAWYRENAR-PLPWRGEKDPYRVLVSEVLLQOTRVEQALPYYRRELEREPTLKALAAAS 66
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                                                                                                                          Similarity
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Similarity 35.1%;
21; Conservative 61
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                                                                                                        Conservative
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DS: 106
Ver. 2.1
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                                                                                                                     27.7%;
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                                                                                                     61;
                                                                                              Score 471.5; DB 4;
Pred. No. 2.8e-39;
il; Mismatches 120;
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Pred. No. 2.8e-39;
1; Mismatches 120;
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Sequence 4982, Application US/09328352 Patent No. 6562958
                                       RESULT 9
US-09-328-352-4982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC FILE REFERENCE: GTC-007
CURRENT ELIUS CONTROL SEPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT ELLING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US/09/134,001C
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
LENGTH: 360
TYPE: PRT
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                               199
                                                                                                                259
                                                                                                                     232 --ERLEGRFOGLYGVPLFPPEELPGREA-----AFGVRSRPLGEVRHALTHRRLRVEV 282
                                                                                                                                                                                      175 LGATYCLPKRPRCGACPLGAFCRGKEAPGRYPAPRKRRAKEERLV---ALVLLGRKGVHL 231
                                                                                                                                                                                                                        139 MSTAFNHPLATYDGNYFRYWSRLNNDYRDIKLQSTRKAFEQELHPYVLKDAGTFNQAMME 198
                                                                                                                                                                                                                                                       118 ASIAFGERVAAVDGNVRRYLSRL--FARESPKEKELFALAQGLLPEGV-DPGVWNQALME 174
                                                                                                                                                                                                                                                                                                             79 SEANEDEVLKYWEGLGYYSRARNFHTAVKEVNNNYDGEVPYDPESFKKLKGVGPYTQAAV 138
                                                                                                                                                                                                                                                                                                                                                         19 SFKKDIEDWFHKNORDMPWRETTNPYYIWLSEVMLOOTOVNTVIDYYYRFIHRFPTIOSL
                                                                                                                                                                                                                                                                                                                                                                                                                                              103;
                                                                                                                                                                                                                                                                                                                                                                                        3 AWRKALLAWYRENARPLPWRGEKDPYRVLVSEVLLQQTRVEQALPYYRRFLERFPTLKAL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307 PVSSFTGCMDEGNALWYNLAQPPSVGLAAPVERLLQQ-LRTGAPV 350
                                                                                      LEKRKEKLLNGMWOFPM--REQTNANDVISDDLGKSIETINEPVFKLKHQFTHLTWEIKV 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 GATVCLPKRPRCGACPL--GAFCRGKEAPGRYPAPRKRRAKEERLVALVLLGRKGVHL--
                                                                                                                                                       LGALVCTPKSPLCLFCPTQEHCEAFHMGTTQELPVKTKSLNKKT1EQKVFLTRNDNGQYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -ERLEGREQGLYGVPLFPPEE-----LPGREAAFGVRSRPLGEVRHALTHRRLRV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEEVLRVWQGAGYYRRAEHLHRLARSVEEL-----PPSFAELRGLPGLGPYTAAAVASIA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 26.1%; Score 443; DB 4; 34.3%; Pred. No. 2.2e-36; tive 56; Mismatches 119
                                                                                                                                                                                                                                                                                                                                                                                                                                   119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-663-023-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4982
LENGTH: 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Applicat. Patent No. 5763178
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 113;
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Best Local
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,950
FILING DATE: 06-MAR-1996
                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CHIRIKJIAN, Jack G.
APPLICANT: COLLIER, G. Bruce
TITLE OF INVENTION: OSCILLATING SIGNAL AMPLIFIER FOR NUCLEIC
TITLE OF INVENTION: ACID DETECTION
                                                        APPLICATION NUMBER: US/01 FILING DATE: 07-JUN-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                    ZIP: 20007-5109
                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                        CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QKEHLAIELEG-----QWLSP-----EQAIAKGVP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVCLPKRPRCGACPLGAFC----RGKEAPGRYPAPRKRRAKEERLVALVLLGRKGVHLER 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GERVAAVDGNVRRVLSRLFARES-----PKEKELFALAQGLLPEGVDPGVWNQALMELGA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLEEVLRVWQGAGYYRRAEHLHRLARSVEE---LPPSFAELRGLPGLGPYTAAAVASIAF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- RRLRVEVRGALWEGEGEDPWKRPLPKLMEKVLRKALP 312
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                                                                                                                                                                                                                                                                          D.C
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                                                                                                                                                                                                                                                                                                             E: Foley & Lardner
3000 K Street, N.W.,
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33.3%;
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Pred. No. 2.6e-36;
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APPLICANT: BAZAR, LEGNARD S.
TITLE OF INVENTION: DETECTION AND MAPPING OF POI
TITLE OF INVENTION: DIGESTION
FILE REFERENCE: 066659/0118
CURRENT APPLICATION NUMBER: US/09/402,959A
CURRENT EILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: PCT/US98/06878
PRIOR FILLING DATE: 1998-04-15
PRIOR FILLING DATE: 1998-04-16
PRIOR APPLICATION NUMBER: 60/043,184
PRIOR FILLING DATE: 1997-04-16
NUMBER: 05 SEQ ID NOS: 10
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US-09-402-959A-10
                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: CHIRIKJIAN, JACK G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09402959A Patent No. 6548247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                          Matches
                                                                                                           Query Match
                                                                                              Best
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                                                                                                                                                                                      ORGANISM: Unknown Organism FEATURE:
                                                                                                                                                                                                                             TYPE: PRT
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LENGTH: 221 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 IICAPRKPKCEKCGMSKLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 FGERVAAVDGNVRRVLSRLFARE----SPKEKELFALAQGLLPEGVDPGVWNQALMELGA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 SEIAKDIKEIGLSNQRAEQLKELARVVINDYGGRVPRNRKAILDLPGVGKYTCAAVMCLA 135
 16
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                     63;
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                                                                                              Similarity
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ILTFWNTDRRDFPWRHTRDPYVILITEILLRRTTAGHVKKIYDKFFVKYKCFEDILKTPK 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEVLRVWQGAGY-YRRAEHLHRLARSV-----EELPPSFAELRGLPGLGPYTAAAVASIA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGKKAAMVDANFVRVINRYFGGSYENLNYNHKALWELAETLVPGGKCRD-FNLGLMDFSA 194
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                                                                                          16.1%; Score 274.5;
31.7%; Pred. No. le-
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RESULT 12
US-09-107-532A-3843

Sequence 3843, Application US/09107532A
PATENT NO. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and TITLE OF INVENTION: NUCLEIC ACID ANI ENTEROCOCCUS FAJ
                                                                                                                                                                                                          NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...27; SEQUENCE DESCRIPTION: SEQ ID NO: 3843: US-09-107-532A-3843
                                                                                                                                               Matches
                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3843:
                                                                                                                                   Local 63;
                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: GTC-012
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                            82
                                                                          31
                                                                                        26 DPYRVLVSEVLLQQ---TRVEQALPYYRRFLERFPTLKALAAASLEEVLRVWQGAGYYR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 7310 CORRESPONDENCE ADDRESS:
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                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 FGERVAAVDGNVRRVLSRLFARE----SPKEKELFALAOGLLPEGVDDGVWNQALMELGA 177
                       RAEHLHRLARSVEE-----LPPSFAELRGLPGLGPYTAAAVASIAFGERVAAVDGNVRRV 136
                                                          NPFELLIAVILSAQATDVSVNKATP----DLFASFPTPDALAEASIDEIILKIKTIGLYRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 SETAKDIKETGLSNORAEQLKELARVVINDYGGRVPRNRKAILDLPGVGKYTCAAVMCLA 135
                                                                                                                                                                                                                                                                                   ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Waltham
STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVCLPKRPRCGACPLGAFC
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                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 Beaver Street
                                                                                                                              11.1%; Score 188; DB 4; I
30.6%; Pred. No. 5.3e-11;
tive 36; Mismatches 79;
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                              DB 4; Length 227;
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Best Local S
Matches 58
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COMPUTER: IBM PC compatible
DEERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,550
FILING DATE: 26-FEB-1997
CLASSIFICATION: 435
NAPP
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US-08-808-550-36
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Patent No. 58
                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: PROHETICAL: NO FRAGMENT TYPE: N-1 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 104 TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                            Local 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Teebor, George APPLICANT: Hilbert, Timothy P. APPLICANT: Hilbert, Timothy P. TITLE OF INVENTION: MAMMALIAN ENDONUCLEASE III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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STATE: New Jerse
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STREET: Floor
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141 -FARESPKEKELFALAQGILPEGVDPGVW---NQALMELGATVCLPKRPRCGACPLGAFC 196
                                                   89 QKTAKILKDDESGDIPDSLDGLCALPGVGPKMANLVMQIAWGECVGIAVDTHVHRISNRL 148
                                                                                                                                                   28 YRVLVSEVLLQQTRVEQALPYYRRFLERFPTLKALAAASLEEVLRVWQGAGYY-RRAEHL 86
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                                                                                                                                                                                                                 Similarity
                                                                        HRLARSVE-----ELPPSFAELRGLPGLGPYTAAAVASIAFGERVA-AVDGNVRRVLSRL 140
                                                                                                                   FQVLVALMLSSQTRDEVNAAAMKRLKDHGLSIGKILEFKVPDLETILCPVGFYKRKAVYL
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5871992
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1 Hackensack Ave, Continental Plaza,
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Pred. No. 7.6e-10;
3; Mismatches 70;
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USES THEREOF
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APPLICANT: Teebor, George W.
APPLICANT: Hibbert, Timothy P.
APPLICANT: Hibbert, Timothy P.
TITLE OF INVENTION: MAMMALIAN ENDONUCLEASE III AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0
FILING DATE: 26-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., Davi
                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
LENGTH: 259 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza,
                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                 Similarity
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                             R 197
                                                                                         -FARESPKEKELFALAQGLLPEGVDPGVW----NQALMELGATVCLPKRPRCGACPLGAFC 196
                                                                                                                        QKTAKILKDDFSGDIPDSLDGLCALPGVGPKMANLVMQIAWGECVGIAVDTHVHRISNRL
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32.0%;
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Pred. No. 1e-09;
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           Search completed: September 15, 2003, 13:54:22 Job time : 32 secs
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US-08-808-550-31
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US-08-808-550-31
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 201-343-1684 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MAMITITLE OF INVENTION: DIAC
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: F
HYPOTHETICAL: NC
FRAGMENT TYPE: N
ORIGINAL SOURCE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David
REGISTRATION NUMBER: 26,74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sin
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188
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                                   179 VCLPKRPRCGACPLGAFCR 197
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                                                                                                                                            YRNKAKNIQKLSKMIIEDYGGEVPRDRDELVKLPGVGRKTANVVVSVAFGVPAIAVDTHV 142
                                                                                                                                                                           YR-RAEHLHRLARSV-----EELPPSFAELRGLPGLGPYTAAAVASIAFGERVAAVDGNV 133
                                                                                                                                                                                                            NPFELVVAVALSAQCTDALVNRVTKTL-----FQKYKRPEDYLAVPLEELQQDIKSIGL 82
                                                                                                                                                                                                                                                 DPYRVLVSEVLLQQ-----TRVEQALPYYRRFLERFPTLKALAAASLEEVLRVWQGAGY 79
HCKAQSPRCAECPLLSLCR
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SLALGEPRAVNDGNV	115 AAVASIAFGERVAAVDGNVRRVLSRLFARESPKEKELFALAQGLLPEGVDPGVWNQALME	57 PTLKALAAASLEEVLRVWQGAGYYRRAEHLHRLARSVEELPPSFAELRGLPGLG :: : : : : : : : :	1 VEAWRKALLAWYRENARPLPWRGEKDDYRVLVSEVLLQQTRVEQALPYYRRFLERF : : : :	Query Match 39.4%; Score 669.5; DB 2; Length Best Local Similarity 46.2%; Pred. No. 9.7e-45; Matches 154; Conservative 48; Mismatches 96; Indels	ile type: DNA ile type: DNA nes: 1-363 <whi> references: GB:AE002060; GB:AE0000513; NID:g6460082; Imental source: strain R1 ccs: DR2285 DR2285 Ssition: 1 Ssition: 1 Samily: A/G-specific adenine glycosylase</whi>	286, 1571-1577, 1999 : Genome sequence of the radioresistant bacterium ence number: A75250; MUID:20036896; PMID:10567266 ston: A75294	<pre>perg, J.F.; Hickey, E.K.; Lam, P.; McDonald, L.; caser, C.M.</pre>	;Species: Deinococcus radiodurans;Date: 03-Dec-1999 #text_change;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change	LT 1 94 specific adenine glycosylase - Deinococcus radiodurans (s	ALIGNMENTS	2 313.5 18.4 286 2 A72682 3 305.5 18.0 215 2 H97084 4 274.5 16.1 221 2 S30312 5 227 13.4 213 2 F72387	0 360 21.2 297 2 CB7149	4 420 24.4 320 2 E./1303 4 414 24.4 312 2 G84305 379 22.3 308 2 T36366 5 750 22.3 308 2 T36366	2 436 25.6 357 2 D82624 3 423 24.9 328 2 F64537	0 442.5 26.0 461 1 441.5 26.0 371	
PARPGAWNEAVMD 195	GVDPGVWNQALME 174	LPPSFAELRGLPGLGPYTA 114 FPQDYAGWLALPGVGPYTA 136	QALPYYRRFLERF 56 : RGLGYYERFLEAF 76	363; 35; Gaps 11;	PIDN:AAF11831.1; PID:g646	Deinococcus radiodurans R1.	Peterson, J.D.; Dodson, R.J Utterback, T.; Zalewski, C.;	ge 08-Dec-2000	train Ri)		probable A/G-speci probable A/G-speci a/G-specific DNA g endonuclease III ·	hypothetical prote probable DNA GLYCO probable DNA glyco	a/g-spectic duent hypothetical prote probable adenine g	-specific	G-specific adeni G-specific adeni	

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RESULT 3

A/G-specific adenine glycosylase CC0377 [imported] - Caulobacter crescentus C; Species: Caulobacter crescentus C; Species: Caulobacter crescentus C; Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001 C; Accession: H87295

R: Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolor n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A; Title: Complete Genome Sequence of Caulobacter crescentus. A; Reference number: A87249; MUID:21173698; PMID:11259647

A; Reference number: A87249; MUID:21173698; PMID:11259647

A; Residues: 1-349 <STO>
A; Residues: 1-349 <STO>
A; Cross references: GB:AE005673; NID:g13421532; PIDN:AAK22364.1; GSPDB:GN00148

C; Genetics:
C; Superfamily: A/G-specific adenine glycosylase
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A: Residues: 1-375 < KUR>
A: Cross-references: GB: AEC08917;
A: Experimental source: strain 169
C: Genetics:
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A; Title: The genome sequence of the facultative intracellular A; Reference number: AD3252; PMID:11756688
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A;Map position: I
C;Superfamily: A/G-specific adenine glycosylase
C;Keywords: glycosidase; hydrolase
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141;
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41; Conservative
                                                                                                                                                                                                                                                                                                                                                                   TQRWPTVLDLAAVEDGDLMAAWAGLGYYARARNLLACARAVANDHGGVFPGTEEGLRALP
                                                                                                                                                                                                       PGVWNQALMELGATVCLPKRPRCGACPLGAFCRG--KEAPGRYPAPRKRRAKEERL-VAL
                                                                                                                                                                                                                                                                                                                     GLGPYTAAAVASIAFGERVAAVDGNVRRVLSRLFARESP---KEKELFALAQGLLPEGVD
                                           LTHRRLRVEVRGALWEGEGEDPWK-----RPLPKLMEKVLRKALPLL
FTHFSLTLRVFAADGANDGDFVWTPREGLGALPSVFLKAAMAAQRLL
                                                                                                                                                                                                                                                                          GVGAYTAAAVAAIAFDRAANVVDGNVERVMSRLFAVEAPMPDSKPELKALAGDLVTDD-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DALRSALLAWYDAQARDLAWRYGPAERRAGVRSDPYRVWLSEVMLQQTTVPHATPYFLSF
                                                                                        VLTRGDEVALVRRPPKGLLGGMLGLPTSDWRTASYDDAEAVA-AAPLAAAWRDLGAVEHV
                                                                                                                                 VLLGRKGVHLERL--EGREQGLYGVPL-----FPPEELPGREAAFGVRSRPLGEVRHA
                                                                                                                                                                               PGDWAQALMDLGATVCKPKGPLCDRCPVSLWCAAYVGGAPETYPRKTKKADRPRRHGVAY
                                                                                                                                                                                                                                                                                                                                                                                                              LERFPTLKALAAASLEEVLRVWQGAGYYRRAEHLHRLARSVEE-----LPPSFAELRGLP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 520; DB 2;
Pred. No. 4.2e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                           314
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                                                                                           302
                                                                                                                                      272
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RESULT 4
AH2674
AH2674
A/G-specific adenine glycosylase mutY [imported] - Agrobacterium tumefaciens
C/Species: Agrobacterium tumefaciens
C/Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam A; Molecule type: DNA A; Residues: 1-367 < KUR> A; Reference number: A; Accession: AH2674 A; Title: The Genome of the A; Reference number: AB2577; A; Experimental source: strain A;Cross-references: GB:AE008688; PIDN:AAL41814.1; A;Status: preliminary circular chromosome
A/G-specific adenine glycosylase Natural Genetic; MUID:21608550; C58 (Dupont) Engineer Agrobacterium PMID:11743193 PID:g17739170; Agrobacterium tumefaciens GSPDB:GN00186 tumefaciens (strain

130; Similarity Conservative 30.3%; Score 515.5; DE 37.1%; Pred. No. 1e-32; 55; Mismatches DB 2; 124; Length Indels 41;

AAWPRVDDLATAPVEDVMAAWAGLGYYARARNLKKCAEAVAREHGGVFPDTEEGLKQLPG ERFPTLKALAAASLEEVLRVWQGAGYYRRAEHLHRLARSVEE-----LPPSFAELRGLPG SYAQMLLAWYDRHHRELPWRTSPAMAARGKRADPYHVWLSEVMLQQTTVQAVKPYFLKFL 128 108 68

IGDYTSAAVAAIAFNRQAAVMDGNVERVISRLFAIDAPLPGSKPAMKAKVAELTP-AERP 165 187

GVWNQALMELGATVCLPKRPRCGACPLGAFCRG--KEAPGRYPAPRKRRAKEERL-VALV GDFAQAMMDLGATICTPKRPACALCPFNGACLALTRDEPERFPVKAAKKAKPVRLGAAFV

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adenine glycosylase (EC 3.2.2.-) NMA1614 [imported] - Neisseria meningitidis C:Species: Neisseria meningitidis C:Species: Neisseria meningitidis C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C:Accession: B81855
R:Parkhill, J: Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Nature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                                                   RESULT
B81855
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A;Acession: F97456
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C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: F97456
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Goodner, B.; Hinkle, G.; Gattung, R;Goodner, R;G
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C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Goodner, B.; Hinkle, G.; Gattung, A.; Liu, F.; Wollam, C.; Allinger, Science 294, 2323-2328, 2001
A; Reference number: A81775; A; Accession: B81855
                           A; Title: Complete DNA sequence of a serogroup A strain of A; Reference number: A81775; MUID:20222556; PMID:10761919
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A; Residues: 1-367 < KUR>
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C:Species: Agrobacterium tumefaciens
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Superfamily: A/G-specific adenine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLGRKGVHLERL---EGREQGLYGVPLFP-PEELPG----REAAFGVRSRPLGEVRHALT
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| : ||:|:||:| || || || ||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYAQMLLAWYDRHHRELPWRTSPAMAARGKRADPYHVWLSEVMLQQTTVQAVKPYFLKFL
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Markelz,
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ckelz, B.;
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A; Molecule type: DNA
A; Residues: 1-349 <PAR>
A; Cross-references: GB:AL162756;
A; Experimental source: serogroup
C; Cenetics:
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C;Superfamily: A/G-specific adenine glycosylase
C;Keywords: glycosidase; hydrolase
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                                   GALW--EGEGEDPWKRP-----LPKLME
                                                                                                                                           GATVCKRTKPLCHQCPMADICEAKKQNRTAELPRKKTAAEVPTLPLYWLIVRNRDGAILL
                                                                                                                                                                             GATVCLPKRPRCGACPLGAFCRGKEAPGRYPAPRKRRAKEE---RLVALVLLGRKG-VHL
                                                                                                                                                                                                                                  QDEVLSLWAGLGYYSRARNLHKAAQQVVEQFGGTFPSERKDLETLCGVGRSTAAAICAFS
                                                                                                                                                                                                                                                                                                                                                               EAQMPSESPSDGIWIKPAHLKDYGLPKPLE
                                                                                                                                                                                                                   FNRRETILDGNVKRVLCRVFARDGNPQDKKFENSLWTLAESLLPSENADMPAYTQGLMDL
                                                                                                                                                                                                                                                                                                                           LEEVLRVWQGAGYYRRAEHLHRLARSVEE-----LPPSFAELRGLPGLGPYTAAAVASIA
                                                                     EKRPAKGIWGGLYCVPCF--ESLNGLSDFAAKFSLTMADMDEQTALTHRLTHRLLLITPF
                                                                                                         ER--LEGRFQGLYGVPLFPPEELPGRE---AAFGVRSRPLGE---VRHALTHRRLRVEVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 503; DB
Pred. No. 8.9e
52; Mismatches
                                   304
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.9e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 349
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A/G-specific adenine glycosylase homolog yfhQ - Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 08-Dec-2000 C;Accession: A69802

R;Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, A.; Aluthors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchlya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Reference number: A65800 MUID:98044033; PMID:9384377

A; Molecule type: DNA A; Residues: 1-369 < KUN> A;Cross-references: A;Status: preliminary; nucleic acid GB: Z99108; GB:AL009126; sequence not shown; NID: g2633055; translation PIDN:CAB12691 not

PID:e11828

A; Experimental C; Genetics:

Superfamily: A/G-specific adenine glycosylase

Query Match 36.1 Best Local Similarity 36.1 Matches 112; Conservative 29.5%; 47; Score Pred. Mismatches 501.5; DB No. 1.2e-31 2; Length Indels 369; 43; Gaps

GSPDB:G

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R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, ri, H.; Qin, H.; Vamathevan, J.; Gill; J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R. A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R. A;Accession: umber: A81000; MUID:20175755; PMID:10710307
A;Accession: D81088
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <TET>
A;Cross-references: GB:AE002488; GB:AE002098; NID:97226631; PIDN:AAF41760.1; PID:97
A;ScenetLos:
A;Gene: NMB1396
C;Superfamily: A/G-specific adenine glycosylase
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DB1088

A/G-specific adenine glycosylase NMB1396 [imported] - Neisseria meningitidis
C/species: Ne
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Best Local S
Matches 130
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                                                                                                                                  GATVCKRTKPLCHQCPMADICEAKKQNRTAELPRKKTAAEVPTLPLYWLIVRNRDGAILL
                                                                                                                                                                           GATVCLPKRPRCGACPLGAFCRGKEAPGRYPAPRKRRAKEE----RLVALVLLGRKG-VHL
                                                                                                                                                                                                                                       FNRRETILDGNVKRVLCRVFARDGNPQDKKFENSLWTLAESLLPSENADMPAYTQGLMDL
                                                                                                                                                                                                                                                                                                                                         QDEVLSLWAGLGYYSRARNLHKAAQQVVRQFGGTFPSERKDLETLCGVGRSTAAAICAFS
                                                                                                                                                                                                                                                                                                                                                                                          LEEVLRVWQGAGYYRRAEHLHRLARSVEE-----LPPSFAELRGLPGLGPYTAAAVASIA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLAWYRENAR-PLPWRGEKDPYRVLVSEVLLQQTRVEQALPYYRRFLERFPTLKALAAAS
                             EKRPAKGIWGGLYCVPCF--ESLNGLSDFAAKFSLTMADMDEQTALTHRLTHRLLLITPF
                                                                               ER---LEGREQGLYGVPLEPPEELPGRE----AAFGVRSRPLGE----VRHALTHRRLRVEVR
                                                                                                                                                                                                                                                                     FGERVAAVDGNVRRVLSRLFARE-SPKEKE----LFALAQGLLP-EGVDPGVWNQALMEL 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.3%; Score 498; DB 2; 39.4%; Pred. No. 2.2e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52;
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                             A; Deduct type: DNA
A; Molecule type: DNA
A; Residues: 1-387 <STO>
A; Cross references: GB: AE005176; PID:g12723767;
A; Cross references: Strain IL1403
A; Experimental source: strain C; Genetics: A; Gene: mutY
                                                                                                                                                                        A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: A86730
                                                                                                                                                                                                                                                     C;Accession: A86730
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Genome Res. 11, 731-753, 2001
                                                                                                                                                                                                                                                                                                                            purine nucleosidase (EC 3.2.2.1) mutY [imported] - Lactococcus lactis subsp. N;Alternate names: A/G-specific adenine glycosylase C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
                                                                                                                                                   A; Status: preliminary
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A; Residues: 1-372 <STO>
A; Cross-references: GB.AP001510; GB:BA0000004; NID:g10173440; PIDN:BAB04650.1;
A; Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Mucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A33650; MUID:20512582; PMID:11058132
A;Scatus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
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C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLIWNIRVYEATVKG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HRRLRVEVRGALWEGEGEDPWKRPLPKLMEK 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LMELGALVCTPTSPGCLLCPVRDHCRAFAAGVQEQLPIKAKKKKPKAKQLIAAVIRNEKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISTFQNDLVTWFSNHYRELPWRENKDPYRVWVSEIMLQQTRVDTVIPYYQAFMRQFPTLE
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36.9%;
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Pred. No. 2.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - VPSLNDK
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                                                                      PIDN: AAK04939.1;
                                                                                                                                                                                                                                                                                   Malarme,
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-350 <PAN>
A;Cross-references: GB:
C;Genetics:
A;Gene: STY3265
C;Superfamily: A/G-spec
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AG0879
A/G-specific adenine glycosylase STY3265 [imported] - Salmonella enterica subsp.
A/G-specific adenine glycosylase STY3265 [imported] - Salmonella enterica subsp.
C/Species: Salmonella-enterica subsp. enterica serovar Typhi
C/Species: Salmonella-enterica subsp. enterica serovar Typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AG0879
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Parkhill, J.; Dougan, G.; Jar
th, T.; Connerton, P.; Cronin,
S.; Moule, S.; O'Gaora, P.
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                                                                        GATVCLPKRPRCGACPL--GAFCRGKEAPGRYPAPRKRRAKEERLVALVLLGRKGVHLER
                                                                                                                                          FGERVAAVDGNVRRVLSRLFARES-PKEKE----LFALAQGLLP-EGVDPGVWNQALMEL
                                                 GAMVCTRSKPKCTLCPLQNGCIAAAHESWSRYPGKKPKQTLPERTGYFLLL----QHNQE
                                                                                                                   LGKHYPILDGNVKRVLARCYAVSGWPGKKEVENTLWTLSEQVTPARGVER--FNQAMMDL
                                                                                                                                                                                      LDEVLHLWTGLGYYARARNLHKAAQQVATLHGGEFPQTFAEIAALPGVGRSTAGAILSLA
                                                                                                                                                                                                             LEEVLRVWQGAGYYRRAEHLHRLARSVE----ELPPSFAELRGLPGLGPYTAAAVASIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIASISFGLAEPAIDGNLMRVTSRLFELDCDISKSSSRKIF----DGYLRKLISKKRPGDF
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-EGREQGLYGVPLFPPE-ELPGREAAFGVRSRPLGEV----
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36.5%;
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39.3%;
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in, A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN:CAD02935.1;
                                                                                                                                                                                                                                                                                                                         Score 491.5; DE Pred. No. 7e-31; 8; Mismatches 1
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Davis,
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, P.; Davies, R.
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 -RHALTHRRLRV--
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                                                                                                                                                                                                                                                                                                                          49;
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                                                             R;Desiraju, V.; Shanabruch, W.G.; Lu, A.L. J. Bacteriol. 175, 541-543, 1993 A;Title: Nucleotide sequence of the Salmonella A;Reference number: A40647; MUID:93123173; PMII A;Accession: A40647
                                                                                                                                                                                    methylation-independent repair protein mutB -
C; Species: Salmonella typhimurium
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A; Residues: 1-350 <D
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 A;Cross-references: GB:M86634;
                                               A; Status: preliminary
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A; Residues: 1-371 <KUR>
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                                                                                                                                                                    Date: 03-May-1994 #sequence_revision
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deno-Tarraga, A.M.; Chillingworth,
il, M.; Rutherford, K.; Simmonds,
Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Genome sequence of Yersinia pestis, the causative A; Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AL590842; PIDN:CAC89795.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VG-specific adenine glycosylase (EC 3.2.2.-) [imported] - Yersinia pestis (strain; Species: Yersinia pestis (strain; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001; Accession: AH0116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: A/G-specific adenine glycosylase; Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEEVLRVWQGAGYYRRAEHLHRLARSV-----EELPPSFAELRGLPGLGPYTAAAVASIA 121
                                                                                                                                                                                                                                    GAMVCTRSKPKCELCPLNIGCMAYANHSWARYPGKKPKQTLPEK-TAWFLLMQNGSQVWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLDWYQHFGRKTLPWQLDKTPYQVWLSEVMLQQTQVATVIPYFQRFMLRFPDIQALAAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLAWYRENAR-PLPWRGEKDPYRVLVSEVLLQQTRVEQALPYYRRFLERFPTLKALAAAS
IVPIWLNTASVRGCMDDGAGLWYNLAQPPSVGLAAPVERLLHQLLKDPL
                                                                                                                                                                          ERLE--GREQGLYGVPLFPPEE------LPGREAAFGVRSRPLGEVRHALTHRRLR
                                                                                                                                                                                                                                                                                               GATVCLPKRPRCGACPL--GAFCRGKEAPGRYPAPRKRRAKEERLVALVLLGRKG--VHL
                                                                                                                                                                                                                                                                                                                                                          LGQHFPILDGNVKRVLARCYAVDGWPGKKEVEGRLWQISEDVTPANGV--GQFNQAMMDL
                                                                                                                                                                                                                                                                                                                                                                                                              FGERVAAVDGNVRRVLSRLFARES-PKEKE----LFALAQGLLP-EGVDPGVWNQALMEL 175
                                                                                                                  EQRPPVGLWGGLFCFPQFAEQEELIHWLQKQGIPANE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MWLPVSSLDACMDEGGALWYNLAQPPSVGLAAPVERLLQQ-LRTGAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDDVLHLWTGLGYYARARNLHKAAQMVVEHHQGEFPTTFDQILALPGIGRSTAGAILSLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                              ---EVRGALWEGEG-----EDP---WKRPLPKLMEKVLRKAL
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35.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 491; DB 2;
Pred. No. 8.2e-31;
8; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PID:g15979021; GSPDB:GN00175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 371
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                                                                                                                  -TQQLTAFRHTFSHFHLD
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NID:g295203; PIDN:AAA27165.1;

PID: g154184

03-May-1994

#text_change

17-Nov-2000

Salmonella

typhimurium

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mutB

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of.

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C;Genetics:
A;Gene: mutb
C;Superfamily: A/G-specific adenine glycosylase
C;Keywords: DNA repair; iron-sulfur protein
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A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1657
A;Accession: AD1657
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-365 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC97028.1; PID:gl6414300; GSPDB:GN00178
A;Cross-references: GB:AL592022; PIDN:CAC97028.1; PID:gl6414300; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A/G-specific adenine glycosylase homolog lin1797 [imported] - Listeria innocua (A/G-species: Listeria innocua (E.Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 (E.Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 (E.Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 (E.Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #seque
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107; Conserv
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                                                                                                  AVASIAFGERVAAVDGNVRRVLSRLFARE----SPKEKELFALAQGLLPEGVDPGVWNQA 171
                                                                                                                                                                                                           SFVNADEADILKAWEGLGYYSRVRNLQTAMKQVMTDFSGEVPSDLTTILSLKGVGPYTAG
                                                                                                                                                                                                                                                                                                             ALAAASLEEVLRVWQGAGYYRRAEHLHRLARSY-----EELPPSFAELRGLPGLGPYTAA 115
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          Conservative
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pred. No. 2.5e-30;
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R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. chardson, D.; Ermolaeva, M.D.; Vannathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers Chardson, D.; Ermolaeva, M.D.; Venter, J.C.; Fraser, C.M.

1. R.R.; Mekalanos, J.J.; Venter, J.C.; Basser, C.M.

1. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

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                                                                                                                                                                                            SVYKKPHAILDGNVKKTLARCFAVEGWPGOKSVENQLWHYAEMHTPK - VDVDKYNQAMMD
                                                                                                                                                                                                                                                IAFGERVAAVDGNVRRVLSRLFARE-----SPKEKELFALAQGLLÞEGVDÞGVWNQALME 174
                                                                                                                                                                                                                                                                                                APQDEVLHFWTGLGYYARARNLHKAAQMVVSEYGGEFPTDLEQMNALPGVGRSTAAAVLS
                                                                                                                                              LGATVCLPKRPRCGACPLGAFCRGKEA--PGRYPAPRKRRAKEERLVALVLLGR-KGVHL
EQRPQSGIWGGLY---CEPQSEIANIQTTIDQRAIGDSTITSQKTLIAFRHTFSHYHLDI
                                             ER---LEGRFOGLYGVPLFPPEELPGREAAFGVRS-----
                                                                                              MGAMICTRSKPKCSLCPVESECLAKQQGNPQEYPGKKPKTDKPVKATWFVMLYHDNAVWL
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2: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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US-09-651-656-38

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US-09-651-656-38

US-09-103-840A-1

1 US-09-138-110-1922

US-09-107-532A-3654

US-09-107-532A-3654

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US-09-107-532A-3654

US-09-107-642-23

US-09-385-028-1

US-09-385-028-1

US-09-385-028-1

US-09-385-028-1

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Sequence 4, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 7, Appli Sequence 76, Appli Sequence 1725, Ap Sequence 1804, Ap Sequence 1804, Ap Sequence 2086, Ap Sequence 2086, Ap Sequence 1, Appli Sequence 234 	340 GCGGCGGCGGTGGCCTCCATCGCCTTCGGGGAACGGGGATGGCGGGGGGGG	280 GAGGAGCTTCCCCCGAGCTTCGCCGAGCCTTCGGGGCCTTCCTGGTCCTCGGCCCTTACACC: 3	235 TACTACCGGCGGGAACACCTCCACCGCCTGGCCCGAAGCGT 2	175 CTGAAGGCCCTGGCCGCGGCTTCCCTGGAAGAGGTCCTTAGGGTCTGGCAGGGGGCGGGC	115 CAGACCCGGGTGGAGCAGGCCCTCCCCTATTACCGCCGCTTTCTGGAGCGCTTTCCCACC	55 CTCCCCTGGCGGGGGAAAAGAACGATCCTTACCGCGTCCTGGTCTCCGAAGGTCCTTCTGCAG	atch 12.9%; Score 125.4; DB 4; Length 963; cal Similarity 54.7%; Pred. No. 2.5e-17; 311; Conservative 0; Mismatches 231; Indels 27;	AMINO ACID SEQUENCES RELATING TO IAGNOSTICS AND THERAPEUTICS ,991A 788	ALIGNMENTS	41 53.8 5.5 7560 4 US-09-754-112A-2 Sequence 42 53.8 5.5 12738 4 US-09-754-112A-1 Sequence 43 53.8 5.5 47981 4 US-09-679-279-1 Sequence 44 52.8 5.4 4257 2 US-08-690-473-1 Sequence 45 52.8 5.4 4257 3 US-09-259-821A-1 Sequence	37 54.8 5.6 1404 4 US-09-252-991A-1725 Sequence 38 54.8 5.6 2208 4 US-09-252-991A-2086 Sequence 39 54.8 5.6 2586 4 US-09-252-991A-1804 Sequence	35 55.6 5.7 53500 4 US-09-266-965-76 Sequence 36 55.2 5.7 2634 3 US-08-941-936-1 Sequence	56.6 5.8 3600 3 US-09-024-429-5 Sequence 55.8 5.7 2681 3 US-08-928-213B-7 Sequence 55.6 5.7 2363 4 US-09-818-780-22 Sequence	56.6 5.8 2889 3 US-09-024-429-4 Sequence 56.6 5.8 3600 1 US-08-9537-002A-5 Sequence 56.6 5.8 3600 3 US-08-863-010-5 Sequence	56.6 5.8 2889 3 US-08-863-010-4 Sequence

353 GCTGGAGCCATCGCCAGCCTGTCGATGGGCCTGCGCGCACCGATCCTCGACGGCAACGTC

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i TYPE: DNA
i ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6886
                       460 CTCGCCCAGGGCCTCCCCCGAGGGCGTGGACCCCGGGGGTGTGG------AAC 507
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                                                                                                                                                              CGGAGGGTCTTCTCCCGCCTCTTCGCCCGGGAAAGCCCCAAGGAGAAGGAGATTTTCGCC
                                                                                                                                                                                                                      GCTGGAGCCATCGCCAGCCTGTCGATGGGCCTGCGCCACCGATCCTCGACGGCAACGTC
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Patent No. 6551795
GENERAL INFORMATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
SEQ ID NO 6739
LENGTH: 1413
TYPE: DNA
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Best Local Simi
Matches 311;
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US-09-252-991A-6739
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ORGANISM: Pseudomonas aeruginosa
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                                            CAGGCCCTCATGGAGCTCGGGGCCACGGTCTGCCTGCCGAAACGGCCCCGTTGCGGGGCCC 567
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Pred. No. 2.6e-17;
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US-09-252-991A-6783
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US-09-489-039A-4788
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 4788
LENGTH: 1551
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APPLICANT: Gary Breton et. al

APPLICANT: GARY Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity Matches 307; Conserv
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                                                                                            TGTGTCCGCTGAGCAACGGCTGCGTGGCCTACGCGAACC 1138
                                                                                                                                                             ACCAGGCGATGATGGATCTCGGGGCAATGGTTTGCACCCGCTCGAAGCCGAAGTGCGAGC 1099
                                                                                                                                                                                           TGAAGCGCGTGCTCGCCCGCTGCTATGCTGTCAGCGGCTGGCCGGGGAAAAAAAGAGGTGG
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Pred. No. 9.2e-15;
0; Mismatches 245
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RESULT 6 US-08-813-574-1

Sequence 1, Application US/08813574
Patent No. 6013473
GENERAL INFORMATION:

APPLICANT: Wei, Ying-Fei
TITLE OF INVENTION: Human MutY
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham
STREET: 709 Swedeland Road

Corporation

COMPUTER READABLE FORM: MEDIUM TYPE: Diskette

STATE: PA COUNTRY: US ZIP: 19406

USA

CITY: King of Prussia

STREET:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6783
LENGTH: 549
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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                                 CTCGCCCAGGGCCTCCTCCCCGAGGGCGTGGACCCG 495
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Pred. No. 1.3e-13;
0; Mismatches 193;
515
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SEQUENCE CHARACTERISTICS:
LENGTH: 1858 base pairs
LENGTH: 100 bairs
ATYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: 11near
MOLECULE TYPE: cDNA
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Best Local S
Matches 299
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APPLICATION NUMBER: 60/013,132

APPLICATION NUMBER: 1996

FILING DATE: 11-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Han, William T

REGISTRATION NUMBER: ATG5000

TELEPHONE: 610-270-5219

TELEPHONE: 610-270-4026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASCSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/813,574
FILING DATE:
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RESULT 7

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US-09-651-656-38
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Patent No. 6340566
GENERAL INFORMATION:
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US-09-650-855-38
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APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
APPLICANT: LAWRENCE LIVERMORE NATIONAL OF SINGLE NUCLEOTIDE
DIVERTION: DETECTION AND QUANTITATION OF SINGLE VARIATIONS, DNA MUTATIONS,
TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
TITLE OF INVENTION NUMBER: US/09/651,656
CURRENT PILING DATE: 2000-08-29
CURRENT PILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PATENTIN VET: 2.1
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Patent No. 6365355
GENERAL INFORMATION:
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
APPLICANT: LAWRENCE CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA
TITLE OF INVENTION: MUTATIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND DNA
TITLE OF INVENTION: MUMATCHES
FILE REFERENCE: IL-10284
FILE REFERENCE:
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TYPE: DNA
ORGANISM: Escherichia coli
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milarity 54.1%;
Conservative (
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Pred. No. 1.9e-09;
0; Mismatches 163;
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; APPLICANT: FİEISCHMAN, ROBERT D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: WHITE, Owen R.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PATENTIN VEY. 2.1
; SEQ ID NO 2
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                                                                                                                                                                                         ; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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US-09-103-840A-2
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                                                                                                               Query Match 8.9%;
Best Local Similarity 50.2%;
Matches 345; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Escherichia
-09-650-855-38
                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                       ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                             LENGTH: 4403765
                                     4022631
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CCTTACCGCGTCCTGGTCTCCGAGGTCCTTCTGCAGCAGACCCGGGTGGAGCAGGCCCTC 138
                                   CTTCTCGCTTGGTATCAGCGATCGCACCGGGATCTGCCCCTGGCGAGAGCCCCGGTGTCAGC 4022690
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                                                                       CTCCTCGCCTGGTACCGGGAAAACGCCCGCCCCCTCCCCTGGCGGGG---GAGAAGGAC
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                                                                                                             Score 86.6; DB 3;
Pred. No. 6.3e-09;
0; Mismatches 309;
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Pred. No. 1.9e-09;
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                                                                                                             Indels
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APPLICANT: WHITE, Owen R.

APPLICANT: PRASER, Claire M.

APPLICANT: VENTER, John C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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                                                   Query Match
Best Local S
Matches 345
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                                                                                                                  O ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
ORGANISM: Mycobacterium tuberculosis
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345; Conserv
ACCGCCGATGTGTTACGCGCCTGGGGCAAGCTGGGCTATCCCAGGCGAGCCAAGCGCTTA
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                                                   8.9%;
llarity 50.2%;
Conservative
                                                    0,
                                                 Score 86.6; DB 3;
Pred. No. 6.3e-09;
0; Mismatches 309;
                                                                                                                                                                                                                                                                                                                  STRAIN ANALYSIS IN MYCOBACTERIUM
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                                                                                 Length 4411529;
                                                    Indels
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PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEG ID NOS: 5322
SEG ID NO 1922
SEG ID NO 1922
IENOTH: 1176
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
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GENERAL INFORMATION: Document al.

APPLICANT: Lynn Doucette-Stamm et al.

APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
Query Match
Best Local Similarity
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US-08-961-527-12/c
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                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                APPLICATION NUMBER: U:
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                               TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 9909 base pairs
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Human Genome Sciences, STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                        TELEPHONE:
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TOPOLOGY:
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linear
                                                                                             (301) 309-8504
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Sequence 46, Application US/09864866
PACENT NO. 6723548
GENERAL INFORMATION:
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SEQ ID NO 46
LENGTH: 968
TYPE: DNA
ORGANISM: Micrococcus luteus
                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                  Query Match 8.3%;
Best Local Similarity 47.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Nguyen, Khoa
TITLE OF INVENTION: DNA REPAIR POLYPEPTIDES AND
FILE REPERENCE: 265.00170101
CURRENT APPLICATION NUMBER: US/09/864,866
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/206,279
PRIOR APPLICATION NUMBER: US 60/206,279
PRIOR FILING DATE: 2000-05-23
NUMBER OF SEQ ID NOS: 49
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APPLICANT: McCullough, Amanu
APPLICANT: Nguyen, Khoa
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   AGGGGGCGGCTACTACCGG--
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Pred. No. 2.7e-08;
0; Mismatches 185;
                                                                                                                                                                                                                                                                                    Score 81.2;
Pred. No. 3e
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US-09-107-532A-3654
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                            INFORMATION FOR SEQ ID NO: 3654:
                                                                                                         PRIJICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILLING DATE: 14 May 1998
APPLICATION NUMBER: 60/081571
FILLING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILLING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 7310
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 TYPE: nucleic acid STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Waltham
STATE: Massachusetts
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                                                                                             TELEFAX: (781)893-8277
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                                      LENGTH: 1212 base pairs
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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RESULT 15
US-09-134-000C-1710
US-09-134-000C-1710
Sequence 1710, Application US/09134000C
Sequence 1710, Application US/09134000C
Sequence 1710, Application US/09134000C
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al ANINO ACID SEQUENCES RELATIVE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FOR DIAGNOSTICS AND TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FOR DIAGNOSTICS AND TITLE APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
PRIOR FILING DATE: 1997-08-15
SEQ ID NO 1710
SEQ ID NO 1710
LENGTH: 1188
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                                    MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
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LOCATION: (B) LOCATION 1...1212
SEQUENCE DESCRIPTION: SEQ ID NO: 3654:
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pred. No. 0.00023;
0; Mismatches 206;
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Search completed: January 20, 2005, 04:39:48 Job time : 134 secs

473

GCCGTTTATTTG

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                    974
112.4
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Match Length DB
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                      11.5
10.7
10.7
9.5
9.1
9.1
8.9
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT NEW PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US07_NEW PUB.seq:*

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8 9 US-09-974-300-1583

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Sequence 4691, Ap
Sequence 1, Appli
Sequence 9, Appli
Sequence 484, App
Sequence 1325, Ap
Sequence 32132, A
Sequence 32132, A
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Sequence 31, Appl
Sequence 21, Appl
Sequence 35788, A
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Sequence 4667, Ap	904	Sequence 1, Appli	19		2		29507,	85	Sequence 1, Appli	Sequence 1, Appli	508	1	23	Sequence 17, Appl	o	23	1, App	Sequence 3, Appli	Sequence 5404, Ap	5759,	5667		42,	3629	3596,	1588	Sequence 1, Appli	4577	Sequence 1, Appli	Sequence 46, Appl	Sequence 12, Appl	Sequence 12, Appl

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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 975
                                                                                                                                       Query Match 99.9%; Score 974; DB 10; 1
Best Local Similarity 100.0%; Pred. No. 3.9e-220;
Matches 974; Conservative 0; Mismatches 0;
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APPLICANT: Yokoyama Shigeyuki
TITLE OF INVENTION: GENE ENCODING DNA REPAIR ENZYME
FILE REFERENCE: PH-1261-US
CURRENT APPLICATION NUMBER: US/09/938,901
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP2001-47762
PRIOR FILING DATE: 2001-02-23
                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Thermus thermophilus FEATURE:
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RESULT 2
US-10-156-761-4691
Sequence 4691, Application US/10156761
PUblication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
INUMBER OF SEQ ID NO 4691
LENGTH: 939
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
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Sequence 1, Application US/10156761
PUBLICATION NO. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: HORIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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LENGTH: 9025608
TYPE: DNA
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NAME/KEY: misc feature
LOCATION: (4187715)
OTHER INFORMATION: a, t,
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Pred. No. 6e-18;
0; Mismatches 306;
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; LENGTH: 1854
; TYPE: DNA
; ORGANISM: Homo &
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US-10-469-992-9
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Publication No. US2040096863A1
GENERAL INFORMATION:
APPLICANT: Livneh, Zvi
APPLICANT: Livneh, Zvi
APPLICANT: Blumenstein, Sara
TITLE OF INVENTION: METHODS AND KITS FOR DETERMINING A RISK TO DEVELOP CANCER, FOR EVI
TITLE OF INVENTION: AN EFFECTIVENESS AND DOSAGE OF CANCER THERAPY AND FOR CORRELATING
TITLE OF INVENTION: ACTIVITY OF A DNA REPAIR ENZYME AND A CANCER
FILE REFERENCE: 26315
CURRENT FILING DATE: 2003-09-16
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1 SEQ ID NO 9
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Best Local Similarity
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GGCCTTCTGCCGGG
                               GGAGCTAGGGGCCACAGTGTGTACCCCACAGCGCCCACTGTGCAGCCAGTGCCCTGTGGA 1033
                                                                                                GGGTCTAGCCCAGCAGCTGGTGGACCCAGCCCGGCCAGGAGATTTCAACCAAGCAGCCAT
                                                                                                                                                                   GTGCCGTGTCCGAGCCATTGGTGCTGATCCCAGCAGCACCCTTGTTTCCCCAGCAGCTCTG
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Pred. No. 2.2e-15;
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TITLE OF INVENTION: Nucleic Acids, Proteins and FILE REFERENCE: PA106
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 484
FUNDS: NUMBER: 1878
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US-09-925-301-484
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Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
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Best Local Similarity
Matches 299; Conserv
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1446)
OTHER INFORMATION: n equals a,t,9,
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Pred. No. 2.2e-15;
0; Mismatches 225;
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S-07-77-300
Sequence 1583, Application US/09974300
Sequence 1583, Application US/09974300
Patent No. US20020146721A1
Patent No. US20020146721A1
Patent No. US20020146721A1
PAPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
APPLICANT: Clausen, Ib Groth
APPLICANT: Clausen, Ib Groth
ITILE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
FILE REFERENCE: 10085.500-US
FILE REPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR PILING DATE: 2001-0-3-27
INUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1583
LENGTH: 528
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TYPE: DNA
ORGANISM: Bacillus licheniformis
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(528)
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TOTHER INFORMATION: n = A,T,C or G
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RESULT 7
US-10-437-963-1325
US-10-437-963-1325
Publication No. US20040123343A1
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: LA ROSA, Thomas J.
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pred. No. 1.2e-12;
0; Mismatches 183;
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RESULT 8
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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_101202C.1
US-10-437-963-1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 1325
LENGTH: 5850
TYPE: DNA
TYPE: DNA
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)
CURRENT APPLICATION INVESE: US
CURRENT APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION AP
                                                                                                                                                                                                                                                                                                                                                                               Sequence 32132, Application US/10425114
Publication No. US20044034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.4%;
Best Local Similarity 54.4%;
Matches 211; Conservative
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Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9;
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; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; FTHER INFORMATION: C
US-10-425-115-92673
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                                                                                         APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE REPERENCE: 38-21(53222)B
FILE REPERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 92673
LENGTH: 1749
                                                                                                                                                                                                                                                                                                                               Sequence 92673, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 282; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGGGTGCCCGTGGTCGCTTACTACGAGCGGTGGATGGCGCGGTGGCCGACCGTACG
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Pred. No. 6.9e-12;
0; Mismatches 253;
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Clone

ID:

MRT4577_184509C.

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FARLICANT: GICQUEL, BRIGITTE
FAPILICANT: GICQUEL, BRIGITTE
FITTLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING MULTIDRUG
FITTLE OF INVENTION: RESISTANT STRAINS OF M. TUBERCULOSIS HAVING MUTATION
FILE REPERENCE: 01345.023-0000
FILE REPERENCE: 01345.023-0000
FILE REPERENCE: 01345.023-0000
FILE REPERENCE: 01345.023-0000
CURRENT APPLICATION NUMBER: US/10/216,817
CURRENT FILING DATE: 2002-11-13
FRIOR APPLICATION NUMBER: 60/311,824
FRIOR APPLICATION NUMBER: 60/311,824
FRIOR APPLICATION NUMBER: 60/313,523
FRIOR APPLICATION NUMBER: 60/313,523
FRIOR APPLICATION NUMBER: 60/313,523
FRIOR FILING DATE: 2001-08-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 6.9e-12;
0; Mismatches 253;
            Score 86.6; DB 15;
pred. No. 3.1e-11;
0; Mismatches 309;
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                                                                                                                                                                                                                                                         Sequence 35788, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.9%;
Best Local Similarity 50.2%;
Matches 345; Conservative
                                                                                                                                                                                          APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                              APPLICANT:
                                                                                                                                                                             APPLICANT:
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Cao, Yongwei
Wu, Wei
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Barbazuk, Brad
Li, Ping
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LENGTH: 1425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
               TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT4530_39677C.1
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                                                             REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                  APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 9410 Ke
CITY: Rockville
                                                                                                                                                                                                    CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Human Genome Sciences, STREET: 9410 Key West Avenue
                                               TELEPHONE:
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                                                  (301) 309-8504
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55.7%;
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Pred. No. 3.6e-11;
0; Mismatches 143;
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-12
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US-10-158-844-12/C

// Sequence 12, Application US/10158844

// Sequence 12, Application US/10158844

// Publication No. US20040029118A1
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Best Local Similarity 52.2%;
Matches 218; Conservative
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APPLICANT: Kunsch et al.
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     INFORMATION
COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

COMPUTER: Dell Lattitude Pentium 3

OPERATING SYSTEM: Windows 98

OPERATING SYSTEM: Windows 98

OPERATING SYSTEM: Windows 98

OPERATING SYSTEM: Windows 98

OPERATING DATE: Text

CURRENT APPLICATION NUMBER: US/10/158,844

APPLICATION NUMBER: US/10/158,844

FILING DATE: 03-Uni-2002

CLASSIFICATION NUMBER: US 08/961,527

APPLICATION NUMBER: US 60/029,960

APPLICATION NUMBER: US 60/029,960

APPLICATION NUMBER: US/0/29,960

FILING DATE: 1996-10-31

ATTORNEY/AGENT TIFORMATION:

NAME: Hyman, Mark J.

REGISTRATION NUMBER: 46,789

REFERENCES/DOCKET NUMBER: PB340P1D1

NORMATION FOR SEQ ID NO: 12:
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NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
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Pred. No.
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Sequence 46, Application US/09864866

Sequence 46, Application US/09864866

Patent No. US20020127656A1

APPLICANT: Lloyd, R. Stephen
APPLICANT: Lloyd, R. Stephen
APPLICANT: NGLYEN, Khoa
APPLICANT: NGLYEN, Khoa
APPLICANT: NGLYEN, Khoa
APPLICANT: NGLYEN, Khoa
CURRENT APPLICATION NUMBER: US/09/864,866

CURRENT APPLICATION NUMBER: US/09/864,866

CURRENT APPLICATION NUMBER: US/09/864,866

CURRENT APPLICATION NUMBER: US/09/864,866

PRIOR APPLICATION NUMBER: US/09/864,866

SEQ ID NO. 46

SEQ ID NO. 46

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386 TGGACGGGAACGTCCGGAGGGTCCTCTCCCGCCTCTTCGCCCGGGAAAGCCCCCAAGGAGA 445
800 CGCGCGCCTGCTGGCCTACGAGCTCAAGCCCCGGCC 835
                                                           626 GGAAGCGCCGGGCGAAGGAGGAGCGCCTCGTCGCCC 661
                                                                                                                   566 CCTGCCCCTAGGGGCCTTCTGCCGGGGGGAAGGAAGGCCCCCGGGGGCGTACCCCGCGCCCA 625
                                                                                                                                                                                                                                          446 AGGAGCTTTTCGCCCTCGCCCAGGGCCTCCCCCGAGGGCGTGGACCCCGGGGGGTGTGGA 505
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Search completed: January 20, 2005, 06:10:40 Job time : 678 secs

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Perfect score:
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Match
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1: /cgn2_6/ptodata/1/

2: /cgn2_6/ptodata/1/

3: /cgn2_6/ptodata/1/
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-09-131-5704-23310
US-09-252-991A-23310
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US-09-108-155-37
US-09-651-656-37
US-09-650-855-37
US-09-650-855-37
US-09-69-134-001C-4684
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US-09-629-222A-36
US-09-629-222A-36
US-09-629-222A-34
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US-08-808-550-37
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Sequence 7308, Ap
Sequence 2115, Ap
Sequence 2, Appli
Sequence 23110, A
Sequence 9, Appli
Sequence 9, Appli
Sequence 37, Appl
Sequence 11959, A
Sequence 11959, A
Sequence 4581, Ap
Sequence 4684, Ap
Sequence 256, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 14, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 35, Appl
Sequence 36, Appl
Sequence 3843, Appl
Sequence 39, Appl
Sequence 31, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 37, Appl
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US-09-252-991A-17572	US-09-252-991A-30904	US-08-808-550-30	US-09-629-222A-33	US-09-489-039A-9560	US-09-492-709A-296	US-09-650-855-25	US-09-651-656-25	US-08-808-550-38	US-08-808-550-29	US-08-808-550-35	US-09-134-000C-3440	US-09-583-110-4518	US-09-134-001C-3225	US-09-710-279-2684	US-09-710-279-972	US-08-808-550-2	US-08-808-550-42
							Sequence 2					Sequence 4	Sequence 3	Sequence 2	Sequence 9	Sequence 2	Sequence 4
17572, A	30904, A		3, Appl		296, App	•	25, Appl	•	29, Appl	Ś	•	4518, Ap	•	2684, Ap	972, App	, Appli	42, Appl

US-09-107-532A-7308

RESULT 1

ALIGNMENTS

Sequence 7308, Application US/09107532A PATENT NO. 563275 GENERAL INFORMATION: APPLICANT: Lynn A Doucette-Stamm and David Bush TITLE OF INFORMATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INFORMATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INFORMATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INFORMATION: NUCLEIC AND THERAPBUTICS NUMBER OF SEQUENCES: 7310 CCRRESPONDENCE ADDRESS: ADDRESSES: GENOME THERAPBUTICS CORPORATION STREET: 100 Beaver Street CTITY: Walatham STATE: Massachusetts COUNTRY: USA TITLE COUNTRY: USA TITLE COUNTRY: USA COMPUTER READABLE FORM: MEDIUM TYPE: CD/ROM ISO9660 COMPUTER READABLE FORM: MEDIUM TYPE: CD/ROM ISO9660 COMPUTER: ASCII COMPUTER: PC OPERATING SISTEM: <UNAVOID-1998 PRICATION NUMBER: 405/09107,532A APPLICATION NUMBER: 60/095,598 PRILING DATE: 10-104-1998 APPLICATION NUMBER: 60/095,598 PRILING DATE: 10-104-1997 APPLICATION NUMBER: 60/095,598 PRILING DATE: 10-104-1997 APPLICATION NUMBER: 60/095,598 PRILING DATE: 10-104-1997 APPLICATION NUMBER: 60/095,598 PRILING DATE: 10-104-1997 ARESISTRATION NUMBER: 60/095,598 PRILING DATE: 0-104-1997 ARESISTRATION NUMBER: 60/095,598 PRILING DATE: 0-104-1998 ARESISTRATION NUMBER: 60/095,598 PRILING DATE: 0-104-1998 ARESISTRATION NUMBER: 60/095,598 ARESISTRA

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APPLICATION DUCCETTE Stamm et al
APPLICANT: LYNN DOUCETTE ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 5115
LENGTH: 395
TYPE: PAT
ORGANISM: Enterococcus faecalis
US-09-134-000C-5115
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US-09-134-000C-5115
US-09-134-000C-5115
; Sequence 5115, Application US/09134000C
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; GENERAL INFORMATION:
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Best Local Similarity 32.7%; Pred. No. 2.3e-42;
Matches 118; Conservative 66; Mismatches 113; Indels
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Best Local (
                                                                                                                                                                                                                                                                                       y Match 28.5%; Score 485; DB 4; Length 395; Local Similarity 33.5%; Pred. No. 2.3e-40; hes 115; Conservative 56; Mismatches 108; Indels 64;
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                                                         LGPYTAAAVASIAFGERVAAVDGNVRRVLSRLFARES----PKEKELFALAQGLLPEGVD 164
                                                                                                                                                                   ERFPTLKALAAASLEEVLRVWQGAGYYRRAEHLHRLARSV-----EELPPSFAELRGLPG 108
                                                                                                                                                                                                                                    EAWRKA-----LLAWYRENARPLPWRGEKDPYRVLVSEVLLQQTRVEQALPYYRRFL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTPTSPKCETCPIQAFCLANKRGIQT--SFPVKTKKAKPKDVYYISAALQNHSGAYYFEE 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLLKAWEGLGYYSRARNIQAAAKQIMSEFDGEMPQTPEEISSLKGIGPYTTGAIASIAFG
                                                                                                                                     EWFPTIQDLAEAPODKLIKAWEGLGYYSRARNIKVAAQQIVSEFGGKMPDTIEDIRSIKG
                                                                                                                                                                                                            EAMSPAKVSSFQEDFLAWYEREKRNLPWRANTDAYRIWISEIMLQQTRVDTVIDYFYRFM
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PGVWNQALMELGATVCLPKRPRCGACPLGAFCRGKEA 201	על 164 DPGVWN :	
YTAGATASTAFGQATGVVDGNVARVLCRVRATGADPSSTLVSQQLWGLAQQLV-DPA 259	Db 201 VGRYTA	н
LGPYTAAAVASIAFGERVAAVDGNVRRVLSRLFARESPKEKELFALAQGLLPEGV 163	Qy 109 LGPYTA	0
REPTIKALAAASLEEVIRVWQGAGYYKKAEHLHKIAKS-VEELPESKAELKGIPG 100 :: : : ::	Oy 55 REPTLE :: : Db 141 KWPTLQ	ם ה
		п о
28.3%; Score 481.5; DB 3; Length 535; 36.5%; Pred. No. 8e-40; ive 46; Mismatches 106; Indels 83; Gaps	Query Match Best Local Similarity Matches 135; Conservat	
y FOR SEQ ID NO: 2: CHARACTERISTICS: : 535 amino acids amino acid sDNESS: single 3Y: linear TYPE: protein		G
REFERENCE/DOCKET NUMBER: ATG50002 TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5219 TELEPAX: 610-270-4026 TELEX	REFERENCE/DOC TELECOMMUNICATI TELEPHONE: 6 TELEFAX: 610 TELEX:	· · · · · · ·
	FILING DATE: ATTORNEY/AGENT NAME: Han, W REGISTRATION	
TION: 536 ATION DATA: N NUMBER: 60/013.132	CLASSIFICATION N	. ~. ~. ~.
4.	CURRENT APPLICA APPLICATION N	
IBM Compatible SYSTEM: DOS PasteRO FOr Windows Version 2 0		
6 B. Diskorto		
G OI FINSSIA .		
SmithKline Beecham Corporation 99 Swedeland Road	ADDRESSEE: S STREET: 709	
QUENCES: 18 CE ADDRESS:	NUMBER OF SEQUE CORRESPONDENCE	
Wei, Ying-Fei ENTION: Human MutY	APPLICANT: Wei	·. ·.
ATION:	; Sequence 2, Application US/UBB1; Patent No. 6013473; GENERAL INFORMATION:	
3	RESULT 3 US-08-813-574-2	σ×
PLVAEEPVNFFTDYETVVWQKRTLGEVVHIFSHLKWHILV 349	307 VTE	닭
AAFGVRSRPLGEVRHALTHRRLRVEV 282	Qy 257	۵
:: : : : : :: IIENKKQEFLLEQRPETGLLANWMLFPIEEISKKQFQQLQKLAQPAETEKQLTLELEP 306	249	.
FRKGVHLERLEGRFQGLYGVPLFPPEELPGRE	222	o
PGDFNQALMDLGSAVCTPTSPKCESCPLQQYCAAYQADKMTAYPVKSKKVKPKDVYYVGT 248	Db 189 PGDFNQ	a

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RESULT 5
US-09-198-452A-421
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US-09-252-991A-23310
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                                     Sequence 421, Application US/09198452A Patent No. 6559294 GENERAL INFORMATION:
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SEQ ID NO 23310
LENGTH: 470
TYPE: PRT
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Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MARC J. RUBENfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-19
PRIOR PILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -09-252-991A-23310
APPLICANT: Griffais, R. TITLE OF INVENTION: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                298
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                                                                                                                                                                                    414 QLAIEPWLVAVEGAPRAVAEGDWLWYNLATPP-RLGLAAPVKKLLKRA 460
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                                                                                                                                                                                                                        RLRVE-----VRGA-----LWEGEGEDPWKRPLPKLMEKVLRKA 310
                                                                                                                                                                                                                                                                 RDGAILLYRRPSSGLWGGLWSLPEL--DDLDGLEPLAARHSLALGERRELSGLTHTFSHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVASIAFGERVAAVDGNVRRVLSRLFARE----SPK-EKELFALAQGLLPEGVDPGVWNQ 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALAAASLEEVLRVWQGAGYYRRAEHLHRLA-----RSVEELPPSFAELRGLPGLGPYTAA 115
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                                                                                                                                                                                                                                                                                                  RKG----VHLERLEGRFQGLYGVPLFPPEELPGREAAFGVRSRPLGEVR-----HALTHR 276
                                                                                                                                                                                                                                                                                                                                              AMMDLGATLCTRSKPSCLLCPLVSGCRAHLLGREAD--YPQPKPRKALPQKRTLMPILAN 355
                                                                                                                                                                                                                                                                                                                                                                                    ALMELGATVCLPKRPRCGACPLGAFCR----GKEAPGRYPAPRKRRA-KEERLVALVLLG 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GRYPAPRKRRAK---EERLVALVL----LGRKGVHLER-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 119;
  genomic sequence and polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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US-08-813-574-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever IIILE OF INVENTION: and treatment of infection FILE REFERENCE: 9710-003-999 CURRENT APPLICATION NUMBER: US/09/198,452A CURRENT FILING DATE: 1998-11-24 NUMBER OF SEQ ID NOS: 6849 SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/08813574 Patent No. 6013473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 117; Conservative
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Best Local (
                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/013
APPLICATION NUMBER: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 375
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Chlamydia
                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/813,574
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wei, Ying-Fei
TITLE OF INVENTION: Huma
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
           NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: AT
                                                                                                                                                                                                                        COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                          CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                  IBM Compatible
SYSTEM: DOS
                                                                                                                                                                                                                                                                     Diskette
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                                                                                                        60/013,132
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Road
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                  ATG50002
                                                                                                                                                                                                                                                                                                                                                                                             Corporation
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610-270-5219

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CURRENT APPLICATION NUMBER: US/09/651,656
CURRENT FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: 60/192,764
PRIOR APPLICATION NUMBER: 2000-03-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PATENTALE PATENTIAL NUMBER: PATENTALE PATENTALE
SEQ ID NO 37
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                                                                                                                                                                                         ; LENGTH: 350
TYPE: PRT
; ORGANISM: Escherichia coli
US-09-651-656-37
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US-09-651-656-37
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                                                                                                   Query Match
Best Local Similarity 35.1
Conservative
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 37, Application US/09651656
PATENT NO. 6340566
GENERAL INFORMATION:
APPLICANT: MCCUTHEN-MALONEY, SANDRA
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
TITLE OF INVENTION: DETECTION AND QUANTITATION OF SINGLE NUCLEOTIDE
TITLE OF INVENTION: POLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTA
TITLE OF INVENTION: DOLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTA
TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
FILE REFERENCE: IL-10689
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SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 27.7%; Score 471.5; DB 3; Best Local Similarity 35.1%; Pred. No. 4.5e-39; Matches 121; Conservative 61; Mismatches 120;
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LEEVLRVWQGAGYYRRAEHLHRLARSVEEL-----PPSFAELRGLPGLGPYTAAAVASIA 121
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                                                                                                             27.7%; Score 471.5; DB 3 35.1%; Pred. No. 4.5e-39; tive 61; Mismatches 120
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                                                                                                                                                 DB 3;
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                                                                                                             Indels
                                                                                                                                             Length 350;
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APPLICANT: MCCUTHEN-MALONEY, SANDRA
TITLE OF INVENTION: CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA
TITLE OF INVENTION: MUTATIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND DNA
TITLE OF INVENTION: MISMATCHES
FILE REFERENCE: IL-10.284
CURRENT APPLICATION NUMBER: US/09/650,855
CURRENT FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: 60/192,764
PRIOR APPLICATION NUMBER: 60/192,764
PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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ORGANISM: Escherichia coli
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PVSSFTGCMDEGNALWYNLAQPPSVGLAAPVERLLQQ-LRTGAPV 350
                                                                         QRPPSGLWGGLYCFPQFADEESLRQWLAQRQIAADNLTQ-LTAFRHTFSHFHLDIVPMWL 306
                                                                                                           -ERLEGRFQGLYGVPLFPPEE-----LPGREAAFGVRSRPLGEVRHALTHRRLRV----
                                                                                                                                                                                                                                                                                                   LDEVLHLWTGLGYYARARNLHKAAQQVATLHGGKFPETFEEVAALPGVGRSTAGAILSLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.7%; Score 471.5; DB 3; 35.1%; Pred. No. 4.5e-39; ative 61; Mismatches 120;
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RESULT 10
US-09-489-039A-11959
; Sequence 11959, Application US/09489039A
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PRIOR FILING DATE: 1998-06-30
PRIOR PRILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 4583
LENGTH: 391
TYPE: PRT
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           CURRENT APPLICATION NUMBER: US/09/489,039A CURRENT FILING DATE: 2000-01-27 PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR FILING DATE: 1999-01-29 NUMBER OF SEQ ID NOS: 14342 SEQ ID NO 11959 LENGTH: 516
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Best Local Similarity
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APPLICANT: Lynn Do
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                                                                                                                                   APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: PATHOO-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
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TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
                                                                                                                              FILE REFERENCE: 2709.2004001
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US-09-543-681A-5315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILITILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 5315

LENGTH: 347
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                                                                                                    116 AVASIAFGERVAAVDGNVRRVLSRLFARES-PKEKE----LFALAQGLLP-EGVDPGVWN
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LGRKGVHLERL--EGRFQGLYGVPLFPP---
                                                                                                                                                                                                                                                         ALAAASLEEVLRVWQGAGYYRRAEHLHRLARSV-----EELPPSFAELRGLPGLGPYTAA 115
                                                                                                                                                                                                                                                                                                 QQFSQVVLDWYHKYGRKTLPWQQEKTPYHVWLSEVMLQQTQVATVIPYFERFIARFPNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGOHYPILDGNVKRVLARCYAVSGWPGKKEVEKRLWDISEEVTPAEGVER -- FNOAMMDL
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                                          QAMMDLGAMVCTRTKPKCELCPLNTGCIAYAHHSWADYPGKKP---KKAIPEKTTYFLIL
                                                                                    QALMELGATYCLPKRPRCGACPLGAFC-----RGKEAPGRYPAPRKRRAKEERLVALVL
                                                                                                                            AILSISIKKPYPIIDGNVKRVLARCYAVEGWPGKKEVENKLWEISEQVTPTKGVE--YFN 183
                                                                                                                                                                                                               ALAKAPLDEVLHLWTGLGYYARARNLHKAAQHIVDKHQGQFPDTFEDVCALPGVGRSTAG
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                                                                                                                                                                                                                                                                                                                                                                                        64; Mismatches 123;
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Pred. No. 2e-37
63; Mismatches
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2e-37;
  -BELPGREAAFGVRSRPLGEVRHALTHRR 277
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FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR PLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4684
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US-09-134-001C-4684
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CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4982
LENGTH: 346
TYPE: ERT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4982
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US-09-328-352-4982
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APPLICANT: LYNN DOUGETTE-Stamm et al
APPLICANT: LYNN DOUGETTE-STAMM ET AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4684, Application US/09134001C Patent No. 6380370
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                                                                                                                                                                                 sequence 4982, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
                                                                                                                          APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
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                                                                                                                                                                                                                                                                                                     259 LEKRKEKLLNGMWQFPM--REQTNANDVISDDLGKSIETINEPVFKLKHQFTHLTWEIKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASIAFGERVAAVDGNVRRVLSRL--FARESPKEKELFALAQGLLPEGV-DPGVWNQALME
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                                                                                                                                                                                                                                                                                                                                 --ERLEGRFQGLYGVPLFPPEELPGREA-----AFGVRSRPLGEVRHALTHRRLRVEV 282
                                                                                                                                                                                                                                                                                                                                                                                               LGATYCLPKRPRCGACPLGAFCRGKEAPGRYPAPRKRRAKEERLV---ALVLLGRKGVHL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEANEDEVLKYWEGLGYYSRARNFHTAVKEVNNNYDGEVPYDPESFKKLKGVGPYTQAAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.0%; Score 443; DB 3; Length 36
34.3%; Pred. No. 3.4e-36;
ative 56; Mismatches 119; Indels
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Best Local
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                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: E.
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PRIOR APPLICATION NUMBER: 09/463,891
PRIOR FILING DATE: 2000-01-28
PRIOR PELICATION NUMBER: PCT/US98/15828
PRIOR PILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/053,936
PRIOR APPLICATION NUMBER: 60/053,936
PRIOR FILING DATE: 1997-07-28
NUMBER OF SEG ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Bellacosa, Alfonso
TITLE OF INVENTION: Methods for Detection of Transition
TITLE OF INVENTION: Single-Nucleotide Polymorphisns
FILE REFERENCE: FCCC 96-21
CURRENT APPLICATION NUMBER: US/09/629,222A
CURRENT FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match
Local Similarity 33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 -LEGRFQGLYGVPLFPPE-ELPGREAAFGVRSRP-LGEVRHALTH-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLEEVLRVWQGAGYYRRAEHLHRLARSVEE----LPPSFAELRGLPGLGPYTAAAVASIAF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALLAWYRENAR-PLPWRGEKDPYRVLYSEVLLQQTRVEQALPYYRRFLERFPTLKALAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GERVAAVDGNVRRVLSRLFARES-----PKEKELFALAQGLLPEGVDPGVWNQALMELGA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALLINGEDQHGRHDLEWQVADDEYKVWVSBIMLQQTQVKTVLQYFDREMERFETVEALGYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QKEHLAIELEG-----QWLSP----EQAIAKGVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QAHGLWGGLFCLFILENEHERLKLSQQFKLQPQPQTFQISHSFTHFTWLLNAHVFHVEPD 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TI CTPKKPLCLYCPMQAHCQAYQQGLEQELPFKKPKKTPPVKTADVLIIQCEDEWFWQQR
HKAAQQVATLHGGKFPETFEEVAALPGVGRSTAGAILSLSLGKHFPILDGNVKRVLARCY
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                                         ARES-PKEKE----LFALAQGLLPE-GYDEGVWNQALMELGATVCLEKRPRCGACPLGAF 195
                                                                                                                                 HRLARSVEEL-----PPSFAELRGLPGLGPYTAAAVASIAFGERVAAVDGNVRRVLSRLF 141
                                                                                                                                                                                       PYKVWLSEVMLQQTQVATVIPYFERFMARFPTVTDLANAPLDEVLHLWTGLGYYARARNL 61
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                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                     22.9%; Score 389.5; DB 4 44.8%; Pred. No. 3.3e-31;
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Pred. No. 4.1e-36;
O; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                    37;
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Sequence 2578, Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARTITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2578
SEQ ID NO 2578
TYPE: PRT
ORGANISM: M.catarrhalis
US-09-540-236-2578
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Search completed: January 20, 2005, 06:10:41 Job time : 29 secs
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US-09-540-236-2578
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                                                                                                                                                                                                                                                                                                                                                166 GVWNQALMELGATVCLPKRPRCGACPLGAFCRGKEAPGRYPAPRKRRAKEE---RLVALV 222
                                                                                                                                                                                                                                                                                                                                                                                                                                       153 RSTAGAIVAMGVKKFGVICDGNVKRVLARHRAVCGDITKSATDKRLWEIATALTPKEYS- 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 PYTAAAVASIAFGERVAAVDGNVRRVLSRLFA-----RESPKEKELFALAQGLLPEGVDP 165
                                                                                                                                                                         329 HDLLHSQLIEILPIPTQTLTAYLRHTLTHVHWHLYGMSICLNNSQFNQINQTLTGLGIDY 388
                                                                                                                                                                                                                       259 FGVRSRPLGEV------RHALTH------285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 SFAKRILTWFELHGRHGLPWQYHHQPSADIYAVWVSEIMLQQTQVVTVLKFFEPFLARFA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 AWRKALLAWYRENAR-PLPWRGEKDP----YRVLVSEVLLQQTRVEQALPYYRRFLERFP 57
                                                                                  LWT---DTPYNLPLPAAMHKLL 407
                                                                                                                                                                                                                                                                                                         LLG---RKGVHLERLEGRFQGLYGVPLFPPEELP------GREAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVQELAVADWQEVASFWAGLGYYARARNIHAGAQQVADFIDTHGRFPETVNEWQAVKGVG 152
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
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            442
389.5
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seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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Match
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                             Copyright
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486
375
469
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474
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                        10 US-09-938-901-2
US-09-925-301-1326
US-10-289-762-421
US-10-425-115-277336
US-10-425-114-68280
US-10-437-963-138271
US-10-629-951-36
US-10-156-761-12241
US-10-156-761-12241
US-10-156-761-13808
US-10-424-599-248081
US-10-629-951-34
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Sequence 2, Appli
Sequence 1326, App
Sequence 421, App
Sequence 277336,
Sequence 68280, A
Sequence 18871,
Sequence 36, Appl
Sequence 12241, A
Sequence 6433, Ap
Sequence 6433, Ap
Sequence 248081,
Sequence 248081,
Sequence 248081,
Sequence 34, Appl
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117.5	118.5	119	120.5	120.5	125.5	125.5	126	128	128	129.5	129.5	130	137.5	145	145	147.5	149	150	155	155	U	163.5	176	J	184.5	191	199	200.5	200.5	200.5	228.5
6.9	7.0	7.0			•		٠	7.5	7.5	٠	٠	٠			٠	8.7		٠	•	•	9.3	9.6	0	0	0	ŗ	:	11.8	:	11.8	13.4
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16	15	<u>بر</u>	15	17	15	16	14	14	14	14	16	15	15	17	9	9	17	15	16	15	14	15	14	11	14	15	9	15	15	15	15
7-963-	-10-425-114-4351	-425-114-6805	-10-425-114-7099	-10-425-115-2168	-10-343-710-7	-10-767-701-6116	-10-369-493-	-10-128-714-812	-10-128-714-312	-10-329-C	2	3-66	511	241	09-912-020-	09-738-626-	-10-425-115	-10-425-114	-10-437-963-11366	-10-424-599		-10-424-599-	-10-369-493-	-408A-90	US-10-156-761-12127	-10-629-951-	-864-866-4	-10-335-977-746	0-335-977-728	-10-335-977-	US-10-335-977-7282
ø	e 4351	æ	e 7099	e 2168	e 71, A	e 6116	e 1329	e 8128,	e 3128,	11, A	Sequence 39640, A	Sequence 246739,	Sequence 33, Appl	Ö.		Sequence 3828, Ap			equenc	150617	e 2113,	e 280749	e 5691,	e 9042, A	e 12:	e 35, App	43, App	Sequence 7461, Ap	1280,	7279,	Sequence 7282, Ap

ALIGNMENTS

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Sequence 2, Application US/09938901

Sequence 2, Application US/09938901

GENERAL INFORMATION:

APPLICANT: Kuramitsu Seiki,

APPLICANT: Kuramitsu Seiki,

TITLE OF INVENTION: GENE ENCODING DNA REPAIR ENZYME

FILE REFERENCE: PH-1861-US

CURRENT APPLICATION NUMBER: US/09/938,901

CURRENT APPLICATION NUMBER: US/09/938,901

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: UP2001-47762

PRIOR APPLICATION NUMBER: JP2001-47762

PRIOR PILING DATE: 2001-02-23

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 325

TYPE: PRT

ORGANISM: Thermus thermophilus

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                                                                                                                                                                                                                                                  Query Match 99.8
Best Local Similarity 99.7
Matches 324; Conservative
                   121
                                                                61
                                                                                                             61
                                                                                                                                                                                  1 MEAWRKALLAWYRENARPLPWRGEKDPYRVLVSEVLLQQTRVEQALPYYRRFLERFPTLK 60
AFGERVAAVDGNVRRVLSRLFARESPKEKELFALAQGLLPEGVDPGVWNQALMELGATVC 180
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                                                                                                                                                                                                                                              99.8%; Score 1697; DB 10;
99.7%; Pred. No. 1.8e-145;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                     Indels
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FEATURE:

NAME/KEY: SITE
LOCATION: (34)
OTHER INFORMATION: Xaa ec
NAME/KEY: SITE
LOCATION: (438)
OTHER INFORMATION: Xaa ec
NAME/KEY: SITE
NAME/KEY: SITE
LOCATION: (447)
OTHER INFORMATION: Xaa ec
US-09-925-301-1326
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PRIOR PILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 1326
LENGTH: 486
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US-09-925-301-1326
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Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA106
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Matches 135;
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Best Local Similarity
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CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 LPKRPRCGACPLGAPCRGKEAPGRYPAPRKRRAKEERLVALVLLGRKGVHLERLEGRFQG
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                                                                                                                                                                                                                                                                                                                                         106
                                                                                                                                                                                                                                                                        166 KWPTLQDLÁSÁSLEEVNQLWAGLGYYSKGRRLQEGÁRKVVÉELGGHMPRTÁETLQQLLPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYGVPLFPPEELPGREAAFGVRSRPLGEVRHALTHRRLRVEVRGALWEGEGEDPWKRPLP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYGVPLFFPEELPGREAAFGVRSRPLGEVRHALTHRRLRVEVRGALWEGEGEDFWKRPLF
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                                                                                                                                                                                                                                                                                             REPTLKALAAASLEEVLRVWQGAGYYRRAEHLHRLARS-VEEL---PPSFAEL---RGLPG
                                                                                                                                                                                                                                                                                                                                                                      AMRKALLAMYRENARPLPWRG------EKDPYRVLVSEVLLQQTRVEQALPYYRRFLE
                                                                                                                                                                                                                                        LGPYTAAAVASIAFGERVAAVDGNYRRYLSRLFA----RESPKEKELFALAQGLLPEGV 163
                                                                                                                                                                                                                                                                                                                                       ÁFRGSLLSWYDQEKRDLÞWRRRAEDEMDLDRRAYAVWVSEVMLQQTQVATVINYYTGWMQ 165
                                                  LEGREQGLYGVP--LFPPEELEGREAAF------GVRSRPLGEVRHALTHRRLRV 280
                                                                                                                                                                                                             VGRÝTAGATÁSTAFGQATGVVDGNVARVLCRVRATGADPSSTLVSQQLWGLAQQLV-DPA
                      NSGLLAGIWEFFSVTWEFSEQLORKALLQELORXAGFLFATHXRHLGEVVHTFSHIKLTY
                                                                                 PNTGQCHLCLPPSEPWDQTLGVVNFPRKASRKPPREESSATCVLEQPGALGAQILLVQRP
                                                                                                                                                RPGDFNQAAMELGATVCTPQRPLCSQCPVESLCRARQRVEQEQLLASGSLSGSPDVEECA 344
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        28.4%; Score 483.5; DB 9; Length 486;
36.5%; Pred. No. 4.5e-35;
tive 46; Mismatches 106; Indels 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  equals any of the naturally occurring
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                                                                                                                     -GRYPAPRKRRAK---EERLVALVL----LGRKGVHLER- 233
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; SEQ ID NO 421
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Chlamydia p
US-10-289-762-421
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                          APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Ott
TITLE OF INVENTION: Nucleic Acid Molecules and Ott
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 277336
LENGTH: 469
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US-10-425-115-277336
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CURRENT FILE REPERENCE: 9710-003-99, 762
CURRENT FILING DATE: 2003-03-27
RUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 28.0%; Score 477; DB 15; Best Local Similarity 38.6%; Pred. No. 1.3e-34; Matches 117; Conservative 44; Mismatches 112;
                                                                                                                                                                                                                                                        Sequence 277336, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
                                                                                                                                                                                                                     APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
ORGANISM: Zea mays
                  TYPE: PRT
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5. US20040006218A1
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                                                                                                                                                                               Other Molecules Associated With
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Sequence 68280, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven B
APPLICANT: Tabaska, Jack E
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US-10-425-114-68280
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SEQ ID NO 68280
LENGTH: 482
TYPE: PRT
ORGANISM: Zea may8
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Best Local Similarity
                                                                                                                                                                                                                                                                               Matches 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION INVESE: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                         AAVASIAFGERVAAVDGNVRRVLSRLFA-RESPKEKELFALAQGLLPEGVD----PGVWNQ 170
                                                                                         TVRSLAAATQEEVNEMWAGLGYYRRARFLLEGAKQIIEKGLFPCTALALREVRGIGDYTA 189
                                                                                                                                     TLKALAAASLEEVLRVWQGAGYYRRAEHLHRLARSVEE---LPPSFAELRGLPGLGPYTA 114
                                                                                                                                                                                   ALRAQLLRWYDAHRRDLPWRCVSGSEEERAYAVWVSEVMLQQTRVPVVVAYYERWMARWP
                                                                                                                                                                                                             AWRKALLAWYRENARPLPWR-----GEKDPYRVLVSEVLLQQTRVEQALPYYRRFLERFP
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GAIASIAFNEVVPVVDGNVIRVISRLYTIADNPKESSTVKRFWDLVGQMVDPLRPGDFNQ
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                                                                                                                                                                                                                                                                                                26.3%; Score 448; DB 15; Length 482; 36.4%; Pred. No. 7.5e-32;
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated FILE REFERENCE: 38-21(53221)B CURRENT FILE APPLICATION NUMBER: US/10/437,963; CURRENT FILING DATE: 2003-05-14; NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 138271
LENGTH: 474
TYPE: PDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
US-10-437-963-138271
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Best Local !
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Oryza sativa FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 ALMELGATYCLPKRPRCGACPLGAFC-----RGKEAPGRYPAPR---KRRAKBERLVAL
                                                                                                                                                                                                                                                                                                            106 LPGLGPYTAAAVASIAFGERVAAVDGNVRRVLSRLFA-RESPKEKELFALAQGLLPEGVD 164
                                                                                                                                                                                                                                                                                                                                                        116 ÝSRWMARWÞTVDSLÁAATQEEVNEMWAGLGÝÝRRÁRFÍLLEGAKQIVEKGEFPCTASTÍRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 VILGRKGV-----HLERL----EGRFQGLYGVPLFPPE----ELPGREAAFG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 AMMELGATLCSKTKPGCSQCPVSSHCQALALSREKSSVQVTDFPRVVPKAKPRSDFAAVC
                                                                                                                                                                                                                    165 ---PGVWNQALMELGATVCLPKRPRCGACPLGAFCRGKEAPGR------YP--APRKR
                                                                                                                                                                                                                                                                                                                                                                                                49 YRRFLERFPTLKALAAASLEEVLRVWQGAGYYRRAEHLHRLARSV---EELPPSFAELRG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                            56 AVRAELLRWYDANRRDLPWRRAAEPPAGSGSGRGEEQRAYAVWVSEVMLQQTRVPVVVDY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 AWRKALLAWYRENARPLPWRGEKDP------YRVLVSEVLLQQTRVEQALPY 48
                                                                                                                                                                         PSRPGDFNQAMMELGATLCSKTKPGCSQCPVSSHCQALALSSQNASVKVTDFPRVVPKAK 295
                                                                                                                                                                                                                                                                VRGIGDYTAGAIASIAFNEVVPVVDGNVVRVISRFYAIPDNPKESSTVKRFWQLTGELVD
                                                                                   PRSDFAAVCVVQIS-----
                                                                                                                             RAKEERLVALVLLGRKGVHLERLEGRFQGLYGVPLFPPEELPGREAAFGVRSRPLGEVRH
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                                  ALTHRRLRVEVRGALWE-----GEGE-DPWKRPLPKLWEKVLRKALPL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
-EEGLLAGIWEFPSVLVNEGKTDTLNR--RKEMDKYLKQLLSI 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.0%; Score 442; DB 16; Length 474; 35.0%; Pred. No. 2.6e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -VRSRPLGEVRHALTHRRLRVEV 282
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                                                                                   OGFGEGI
                                                                                     ----AEAEGKDNLFLLIKRP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 70;
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With

RESULT 7 US-10-629-951-36

Sequence 36,

Application US/10629951

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TITLE OF INVENTION: Wethods for Detection of Transition
TITLE OF INVENTION: Single-Nucleotide Polymorphisns
FILE REFERENCE: FCCC 96-21
CURRENT APPLICATION NUMBER: US/10/629,951
CURRENT FILING DATE: 2003-07-29
PRIOR APPLICATION NUMBER: US/09/629,222A
PRIOR APPLICATION NUMBER: US/09/629,222A
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 09/463,891
PRIOR FILING DATE: 2000-07-28
PRIOR PILING DATE: 1907-07-28
PRIOR APPLICATION NUMBER: PCT/US98/15828
PRIOR APPLICATION NUMBER: PCT/US98/15828
PRIOR APPLICATION NUMBER: 00/053,936
PRIOR APPLICATION NUMBER: 00/053,936
PRIOR APPLICATION NUMBER: 1907-07-28
PRIOR APPLICATION NUMBER: 1907-07-28
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; TYPE: PRT
; ORGANISM: E.
US-10-629-951-36
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                                             ORGANISM: Streptomyces avermitilis US-10-156-761-12241
                                                                                                                                                                                                                                  APPLICANT: SHIBA, TAAAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
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GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 36
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12241, Application US/10156761 publication No. US20030119018A1 GENERAL INFORMATION:
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                                                                                                              PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12241
LENGTH: 313
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 AVSGWPGKKEVENKLWSLSEQVTPAVGVER--FNQAMMDLGAMICTRSKPKCSLCPLQNG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 C 196
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HORIKAWA, HIROSHI
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       22.2%;
       Score 377;
          DB 14;
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       Length 313;
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APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATELSHI, NAOKO
APPLICANT: SENCH, AKHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
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PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
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US-09-738-626-6433
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SOTWARE PATENTIN VET. 3.0
SEQ ID NO 6433
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publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAMA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Matches 97; Conservative 32; Mismatches 88
                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                        Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                   LENGTH: 293
TYPE: PRT
                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 LLAVL 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ALAAASLEEVLRVWQGAGYYRRAEHLHRLARSVEE-----LPPSFAELRGLPGLGPYTAA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 BAWRKALLAWYRENARPLPW-RGEKDPYRVLVSEVLLQQTRVEQALPYYRRFLERFPTLK
                               114 AAAVASIAFGERVAAVDGNVRRVLSRLFARE---SPKEKELFALAQGLLPEGVDPGVWNQ 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97;
                                                                        62
                                                                                                     59 LKALAAASLEEVLRVWQGAGYYRRAEHLHRLA-----RSVEELPPSFAELRGLPGLGPYT 113
                                                                                                                                                                                                                        99;
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                                                                                                                                            ARÁVAAFHFGQRVPVVDTNVRRVYQRAVAGRYLAGPAKKQELIDVSLLLENTHAP-EFSA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIZOGUCHI, HIROSHI
ANDO, SEIKO
                                                                      PEDFANASTDEILRSWGKLGYPRRALRIKECAEVIVEKHAGEVPDTVEALLALPGIGDYT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAYASHI, MIKIRO
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                                                                                                                                                                                                                    21.5%; Score 365; DB 9; 1 ilarity 34.6%; Pred. No. 1.3e-24; Conservative 47; Mismatches 120;
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                                                                                                                                                                                                                                                               Length 293;
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RESULT 11
US-10-424-599-248081
; Sequence 248081, Application US/10424599
; Publication No. US20040031072A1
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US-10-437-963-103808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽
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LENGTH: 1719
TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 103808, Application US/10437963 Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)..(1719)
OTHER INFORMATION: unBure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEATURE:
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                   164 DPGVWNQALMELGATVCLPKRPRCGACPLGAFCRGKEAPGRYPAPRKRR-----A
                                                                                                                                                                                                                                                                                                                                                                                      105 GLPGLGPYTAAAVASIAFGERVAAVDGNVRRVLSRLFA-RESPKEKELFALAQGLLPEGV 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 LIMDVLRNATAPVPLSAIDVVWPDDAQRSRALFSLIEDGLAEQNEA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 VHLERLEGRFQ--GLYGVPLFPPEELPGREAAFGVRSRPLGEVRHA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YYRRFLERFPTLKALAAASLEEVLRVWQQAGYYRRAEHLHRLARSV---EELPPSFAELR
                                                                                                                                                           FGVRSRPLGE 268
                                                                                                                                                                                                                                                                                                                                                                                                                                        YYSRWMARWPTVDSLAAATQEEVNEMWAGLGYYRRARFLLEGAKQIVEKGEFPRTASALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVRAELLRWYDANRRDLPWRRAAEPAGSGSGSGSGEEKRAYAVWVSEVMLQHTRVPVVVD 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AWRKALLAWYRENARPLPWR-------GEKDPYRVLVSEVLLQQTRVEQALP
                                                                                                                      RG-RARERAE
                                                                                                                                                                                                   RAARLAAAELAAARAEAEAEAAEDAARAAEVEVETLRSSINGSIAGDITADREL--EELA
                                                                                                                                                                                                                                        KEERLVALVLLGRKG------VHLERLEGRFQGLYGVPLFPPEELPGREAA 258
                                                                                                                                                                                                                                                                              -----SSTV---KR--
                                                                                                                                                                                                                                                                                                                                                           EVRGIGDYTAGAIASIAFNEVVPVVDGNV-RVISRLYAIPDNPKE---------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhou,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALMELGATVCLPKRPRCGACPLGAFCRGKEAPGRYPAPRKRRAKEERLVALVLLGR--KG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wu, Wei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.8%;
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Pred. No. 4
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                                                                                                                                                                                                                                                                              ---FCTRRQQDAELAAAEERRRATARTGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.6e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1719;
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US-10-629-951-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 248081
LENGTH: 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34, Application US/10629951
Publication No. US20040018550A1
GENERAL INFORMATION:
APPLICANT: Bellacosa, Alfonso
TITLE OF INVENTION: Methods for Detection of Transition
TITLE OF INVENTION: Single-Nucleotide Polymorphisns
FILE REFERENCE: FCCC 96-21
                                                                                                                                                                                                                                                                                                                                SEQ ID NO 34
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Best Local Similarity
                                                                                                                                                                            Query Match
Best Local
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PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: PCT/US98/15828
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/053,936
PRIOR APPLICATION NUMBER: 60/053,936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/629,951
CURRENT FILING DATE: 2003-07-29
                                                                                                                                                                                                                                                              LENGTH: 188
TYPE: PRT
ORGANISM: M.
                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1997-07-28
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US/09/629,222A PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Glycine max FEATURE:
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                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 YTS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 YTA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 WPTIHHLAQASLEEVNEMWAGLGYYRRARFLLEGAKKIVAEGGQIPKVASMLRNIPGIGE
85 HIHRLARSV-----EELPPSFAELRGLPGLGPYTAAAVASIAFGERVAAVDGNVRRVLSR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 FPTLKALAAASLEEVLRVWQGAGYYRRAEHLHRLARSV----EELPPSFAELRGLPGLGP 111
                                                                                                          26 DPYRVLVSEVLLQQTRVEQALPYYRRFLERFPTLKALAAASLEEVLRVWQGAGY-YRRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 RVALLDWYDLNRRDLPWRTTFKQEDEEVERRAYGVWVSEVMLQQTRVQTVIAYYNRWMQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 RKALLAWYRENARPLPWRG------EKDPYRVLVSEVLLQQTRVEQALPYYRRFLER 55
                                                                    DPYVILITEILLRRTTAGHVKKIYDKFFVKYKCFEDILKTPKSEIAKDIKEIGLSNQRAE
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                                                                                                                                                                          14.1%; Score 240.5; DB : 32.0%; Pred. No. 1.5e-13
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Pred. No. 1.2
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                                                                                                                                                                                                DB 15;
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                                                                                                                                                        Indels
                                                                                                                                                                                              Length 188;
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LOCATION: (B) LOCATION 1...230

SEQUENCE DESCRIPTION: SEQ ID NO: 7283:
US-10-335-977-7283
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US-10-335-977-7283
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                                                                                                                                                                       Query Match
Best Local S
Matches 66
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Publication No. US20040052799A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 7283:
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/993,002 FILING DATE: 17-DEC-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: GTN-018 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 10031 CORRESPONDENCE ADDRESS:
                                          155 AQGLLPEGVDPGV------
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                                                                                                                                                                         66;
54 -----GLDPNIHAKDLQIKANDFLNLNESFNHNQALIDLGALICSPK-PKCAICPFNP 105
                                                                                                        95 ELPPSFAELRGLPGLGPYTAAAVASIAFGERVAAVDGNVRRVLSRLFARESPKEKELFAL 154
;|| ; | |||;| ||| || ||; | || || |||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                  7 QLPNDYQSLLKLPGIGAYTANAILCFGFREKSACVDANVKRVLLRLF
                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFARE----SPKEKELFALAQGLLPEGVDPGVWNQALMELGATVCLPKRPRCGACPLGAF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLKELARVVINDYGGRVPRNRKAILDLPGVGKYTCAAVMCLAFGKKAAMVDANFVRVINR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
                                                                                                                                                                         Conservative
                                                                                                                                                                                             13.8%;
30.6%;
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                                                                                                                                                                       32;
                                                                                                                                                                     Score 234; DB 15;
Pred. No. 7.7e-13;
2; Mismatches 54;
                                     -----WNQALMELGATVCLPKRPRCGACPLGA 194
                                                                                                                                                                                                           Length 230;
                                                                                                                                                                       Indels
                                                                                                                                                                     64;
                                                                                                                                                                     Gaps
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NAME/KEY: misc_feature;
LOCATION: (B) LOCATION 1...187;
SEQUENCE DESCRIPTION: SEQ ID NO: 7282:
US-10-335-977-7282
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                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7282, Fublication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 7282:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/93,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10
FILING DATE: 30-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
155 AQGLLPEGVDPGV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 FCRGKEAPGRYPAPRKRR-AKEERLVALVLLGRKGVHLERLEGRFQGLY-GVPLFP----
                                                            63
                                                                                                                                                             162 NLEFKLPF------LGTIKHSHTKFKLNLNL 186
                                                                                                                                      16 QLPNDYQSLLKLPGIGAYTANAILCFGFREKSACVDANVKRVLLRLF------
                                                        -----GLDPNIHAKDLQIKANDFLNLNESFNHNQALIDLGALICSPK-PKCAICPFNP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --PEELPGREAAFGVRSRPLGEVRHALTHRRLRVEV 282
                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YCLGKNHLERHTLKKKQEIIQEERYLGVVIQNNQ-IALEKIE---QKLYLGMHHFPNLKE 161
                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/10335977 . US20040052799A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boston
                                                                                                                                                                                                               13.4%; Score 228.5; DB 1 33.5%; Pred. No. 1.9e-12; tive 25; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/10/335,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTN-018
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                                                                                            ----WNOALMELGATVCLPKRPRCGACPLGA 194
                                                                                                                                                                                                                                                     DB 15;
                                                                                                                                                                                                               45;
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                   Length 187
                                                                                                                                                                                                               47;
                                                                                                                                                                                                               Gaps
                                                                                                                                                                             154
                                                                                                                                      62
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115 YCLGKNHLERHTLKKKQEIIQEERYLGVVIQNNQ-IALEKIE---QKLYLGMHHFP 166

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;
INAME/KEY: misc_feature
;
LOCATION: (B) LOCATION 1...98
;
SEQUENCE DESCRIPTION: SEQ ID NO: 7279:
US-10-335-977-7279
Search completed: January 20, 2005, 06:16:04 Job time : 82 secs
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US-10-335-977-7279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
PRIOR APPLICATION NUMBER: 08/993,002
PILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELESPHONE: (617) 227-7400
TELESPAX: (617) 722-4214
INFORMATION FOR SEQ ID NO: 7279:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 maino acids
TYPE: amino acids
TYPE: amino acids
TYPE: protein
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7279, Application US/10335977

Publication No. US20040052799A1

Publication No. US20040052799A1

GENERAL INFORMATION:

APPLICANT: DOUGLAS SMITH et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

RELATING TO HELICOBACTER PYLORI FOR

DIACKOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 10031
                                                                                                                                                                                                                                                                                                   Query Match 11.8%; Score 200.5; DB 15; Length 98; Best Local Similarity 48.4%; Pred. No. 2.8e-10; Matches 45; Conservative 14; Mismatches 29; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 0219-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                   61
                                                                                                                                56 FPTLKALAAASLEEVLRVWQGAGYYRRAEHLHR 88
                                                                                                                                                                                                  1 LETLHNALLKWYEEFGRKDLPFRNLKGINAPYEVYISEVMSQQTQISTVIERFYPPFLKA 60
                                                                                                                                                                                                                                              1 MEAWRKALLAWYRENAR-PLPWR---GEKDPYRVLVSEVLLQQTRVEQALP-YYRRFLER 55
                                                                                              FPTLKDLANAPLEEVLLLWRGLGYYSRAKNLKK 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                   5.
                                                                                                                                                                                                                                                                                                   Gaps
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